



Ana- A

~~HS~~

- 1 -

SEQUENCE LISTING

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Wang, Dunrui

<120> MATERIALS AND METHODS RELATING TO LIPID METABOLISM

<130> 28110/35915A

<140> US/09/835,996

<141> 2001-04-16

<150> US 60/197,137

<151> 2000-04-14

<150> US 09/714,936

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<151> 2000-09-22

<150> US 09/631,451

<151> 2000-08-03

<150> US 09/598,042

<151> 2000-06-20

<160> 45

<170> PatentIn version 3.0

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<222> (46)..(1143)

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<221> misc feature

<222> (1758)

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ctc cca cag gac ccg gtg ggc atg cgg cgg cag ctg cag gag gag ttg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu Gln Glu Glu Leu 85 90 95 100	345
gag gag gtg aag gct cgc ctc cag ccc tac atg gca gag gcg cac gag Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala Glu Ala His Glu 105 110 115	393
ctg gtg ggc tgg aat ttg gag ggc ttg cgg cag caa ctg aag ccc tac Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln Leu Lys Pro Tyr 120 125 130	441
acg atg gat ctg atg gag cag gtg gcc ctg cgc gtg cag gag ctg cag Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val Gln Glu Leu Gln 135 140 145	489
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ggc gtg gac gag gct tgg gct ttg ctg cag gga ctg cag agc cgc gtg Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu Gln Ser Arg Val 165 170 175 180	585
gtg cac cac acc ggc cgc ttc aaa gag ctc ttc cac cca tac gcc gag Val His His Thr Gly Arg Phe Lys Glu Leu Phe His Pro Tyr Ala Glu 185 190 195	633
agc ctg gtg agc ggc atc ggg cgc cac gtg cag gag ctg cac cgc agt Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu Leu His Arg Ser 200 205 210	681
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Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro Asp Pro Gln Met	
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ctc tcc gag gag gtg cgc cag cga ctt cag gct ttc cgc cag gac acc	921
Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe Arg Gln Asp Thr	
280 285 290	
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Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp Gln Glu Thr Glu	
295 300 305	
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Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Gly His Ser Ala Phe	
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gcc cca gag ttt caa caa aca gac agt ggc aag gtt ctg agc aag ctg	1065
Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val Leu Ser Lys Leu	
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Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr His Ser Leu His	
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gac cag ggc cac agc cat ctg ggg gac ccc tgaggatcta cctgcccagg	1163
Asp Gln Gly His Ser His Leu Gly Asp Pro	
360 365	
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Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys
35 40 45

Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu
50 55 60

Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser
65 70 75 80

Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu
85 90 95

Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala
100 105 110

Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln
115 120 125

Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val
130 135 140

Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala
145 150 155 160

Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu
165 170 175

Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His
180 185 190

Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu
195 200 205

Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu
210 215 220

Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys
225 230 235 240

Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu
245 250 255

Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro
260 265 270

Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe
275 280 285

Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp
290 295 300

Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Gly
305 310 315 320

His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val
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His Ser Leu His Asp Gln Gly His Ser His Leu Gly Asp Pro
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tcaacattca gcagaggccc cagatcagcg tctgagccag gccacaatg accaaggagg 180
atg gga tcc tgg gtg cag ctc atc aca agc gtc ggg gtg cag caa aac 228
Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn
1 5 10 15
cat cca ggc tgg aca gtg gct gga cag ttc caa gaa aag aaa cgc ttc 276
His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe
20 25 30
act gaa gaa gtc att gaa tac ttc cag aag aaa gtt agc cca gtg cat 324
Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
35 40 45
ctg aaa atc ctg ctg act agc gat gaa gcc tgg aag aga ttc gtg cgt 372
Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
50 55 60
gtg gct gaa ttg ccc agg gaa gaa gca gat gct ctc tat gaa gct ctg 420
Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
65 70 75 80
aag aat ctt aca cca tat gtg gct att gag gac aaa gac atg cag caa 468
Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln
85 90 95

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tac aca agg tca gca gaa ctc aca gcc agc agg ctg act gca acc agc Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser 195 200 205	804
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aat gtg ctt tcc ttt gca ctt gat ttt gac gaa gcc aca aaa atg att Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile 225 230 235 240	900
gcg aat gat gtc cat aca ctc agg aga tct aaa gcc act gtt gga cgc Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg 245 250 255	948
cct ttg att gct tgg cga tat gta cct ata aat gtt gtt gag aca ctg Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu 260 265 270	996
aga aca cgt ggg gcc ccc acc cgg ata gtg aga aaa gta gcc cgg aac Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn 275 280 285	1044
ctg ggc aag gcc act tca ggt gtc ctt gtt gtg ctg gat gta gtc aac Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn 290 295 300	1092
ctt gtg caa gac tca ctg gac ttg cac aag ggg gca aaa tcc gag tct Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser 305 310 315 320	1140
gct gag tcgctgaggc agtgggctca ggagctggag gagaatctca atgagctcac Ala Glu	1196
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Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
35 40 45

Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
50 55 60

Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
65 70 75 80

Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln
85 90 95

Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile
100 105 110

Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn
115 120 125

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser
130 135 140

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe
145 150 155 160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly
165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr
180 185 190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser
195 200 205

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro
210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile
225 230 235 240

Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg
245 250 255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu
260 265 270

Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn
275 280 285

Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn
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Met Ala Gly Val Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys
15 20 25

atg gtc aag caa gtg act ggg aaa atg ccc atc ctc tcc tac tgg ccc 146
Met Val Lys Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro
30 35 40

tac ggc tgt cac tgc gga cta ggt ggc aga ggc caa ccc aaa gat gcc 194
Tyr Gly Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala
45 50 55

acg gac tgg tgc tgc cag acc cat gac tgc tgc tat gac cac ctg aag 242
Thr Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
60 65 70 75

acc cag ggg tgc ggc atc tac aag gac tat tac aga tac aac ttt tcc	290
Thr Gln Gly Cys Gly Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser	
80 85 90	
cag ggg aac atc cac tgc tct gac aag gga agc tgg tgt gag cag cag	338
Gln Gly Asn Ile His Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln	
95 100 105	
ctg tgt gcc tgt gac aag gag gtg gcc ttc tgc ctg aag cgc aac ctg	386
Leu Cys Ala Cys Asp Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu	
110 115 120	
gac acc tac cag aag cga ctg cgt ttc tac tgg cgg ccc cac tgc cgg	434
Asp Thr Tyr Gln Lys Arg Leu Arg Phe Tyr Trp Arg Pro His Cys Arg	
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Gly Gln Thr Pro Gly Cys	
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Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly Cys His Cys
35 40 45

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Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr Asp Trp Cys Cys
50 55 60

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Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys Thr Gln Gly Cys Gly
65 70 75 80

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Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser Gln Gly Asn Ile His
85 90 95

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Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln Leu Cys Ala Cys Asp
100 105 110

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Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu Asp Thr Tyr Gln Lys
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aag gag aga gac tgc acc tct gag ctt gct ctg gaa ctc att gac cgc Lys Glu Arg Asp Cys Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg 240 245 250	892
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 480 485 490

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 495 500 505

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 Phe Thr His Ser Lys Glu His Tyr His Phe Tyr Glu Ile Ser Ser Phe
 510 515 520

tct gaa acc aag gcc aag cgc ctc atc aag gag gct ggc aat gag ttt 1756
 Ser Glu Thr Lys Ala Lys Arg Leu Ile Lys Glu Ala Gly Asn Glu Phe
 525 530 535

gtg cag cac aat act cgg cag tta agc cgt gtg tat ccc agc ggc ctg 1804
 Val Gln His Asn Thr Arg Gln Leu Ser Arg Val Tyr Pro Ser Gly Leu
 540 545 550 555

agg aca ggc tct tcc atc tac aac ccg cag gga tac 1840
 Arg Thr Gly Ser Ser Ile Tyr Asn Pro Gln Gly Tyr
 560 565

<210> 8
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ala Ser Leu Leu Gln Asp Gln Leu Thr Thr Asp Gln Asp Leu Leu
 1 5 10 15

Leu Met Gln Glu Gly Met Pro Met Arg Lys Val Arg Ser Lys Ser Trp
 20 25 30

Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn Asp Gly Met Thr Val Trp
 35 40 45

His Ala Arg Gln Ala Arg Gly Ser Ala Lys Pro Ser Phe Ser Ile Ser
 50 55 60

Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser Glu Leu Leu Arg Ser
 65 70 75 80

Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe Thr Ile Val Phe His
 85 90 95

Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn Ser Val Glu Glu Ala
 100 105 110

Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val Asp Leu Val Thr Ser
 115 120 125

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln
130 135 140

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln
145 150 155 160

Arg Leu Leu His Leu Met Asn Val Glu Met Asp Gln Glu Tyr Ala Phe
165 170 175

Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly
180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val
195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu
210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Glu Gln Lys Glu Arg Asp Cys
225 230 235 240

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp
245 250 255

Ser Gly Lys Leu Arg His Val Pro Ser Met Asp Gly Phe Leu Ser Tyr
260 265 270

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile
275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser
290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val
305 310 315 320

Glu Gly Tyr Ile Arg Ala Leu Lys Arg Gly Cys Arg Cys Val Glu Val
325 330 335

Asp Val Trp Asp Gly Pro Ser Gly Glu Pro Val Val Tyr His Gly His
340 345 350

Thr Leu Thr Ser Arg Ile Leu Phe Lys Asp Val Val Ala Thr Val Ala
355 360 365

Gln Tyr Ala Phe Gln Thr Ser Asp Tyr Pro Val Ile Leu Ser Leu Glu
370 375 380

Thr His Cys Ser Trp Glu Gln Gln Gln Thr Met Ala Arg His Leu Thr
385 390 395 400

Glu Ile Leu Gly Glu Gln Leu Leu Ser Thr Thr Leu Asp Gly Val Leu
405 410 415

Pro Thr Gln Leu Pro Ser Pro Glu Glu Leu Arg Arg Lys Ile Leu Val
420 425 430

Lys Gly Lys Lys Leu Thr Leu Glu Glu Asp Leu Glu Tyr Glu Glu Glu
435 440 445

Glu Ala Glu Pro Glu Leu Glu Glu Ser Glu Leu Ala Leu Glu Ser Gln
450 455 460

Phe Glu Thr Glu Pro Glu Pro Gln Glu Gln Asn Leu Gln Asn Lys Asp
465 470 475 480

Lys Lys Lys Lys Ser Lys Pro Ile Leu Cys Pro Ala Leu Ser Ser Leu
485 490 495

Val Ile Tyr Leu Lys Ser Val Ser Phe Arg Ser Phe Thr His Ser Lys
500 505 510

Glu His Tyr His Phe Tyr Glu Ile Ser Ser Phe Ser Glu Thr Lys Ala
515 520 525

Lys Arg Leu Ile Lys Glu Ala Gly Asn Glu Phe Val Gln His Asn Thr
530 535 540

Arg Gln Leu Ser Arg Val Tyr Pro Ser Gly Leu Arg Thr Gly Ser Ser
545 550 555 560

Ile Tyr Asn Pro Gln Gly Tyr
565

<210> 9

<211> 1384

<212> DNA

<213> Homo sapiens

<400> 9

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gaaaaaataa atgcagatgt tggaccatgt tggaaacctt gtcaagacag tggattgtct 180

cacacagaat ggaaatgtgg cttctgattc tgggtggcgta tatgttccag agaaatgtga 240

attcagtaca tatgccaaact aaagctgtgg acccagaagc attcatgaat attagtga 300

tcatccaaca tcaaggctat cctgtgagg aatatgaagt cgcaactgaa gatgggtata 360
tcctttctgt taacaggatt cctcgaggcc tagtgcaacc taagaagaca ggttccaggc 420
ctgtggtgtt actgcagcat ggcctagttg gaggtgctag caactggatt tccaacctgc 480
ccaacaatag cctgggcttc attctggcag atgctggttt tgacgtgtgg atggggaaca 540
gcaggggaaa cgcttggctc cgaaaacaca agacactctc catagaccaa gatgagttct 600
gggctttcag ttatgatgag atggctaggt ttgaccttcc tgcagtgata aactttattt 660
tgcagaaaac gggccaggaa aagatctatt atgtcggcta ttcacagggc accaccatgg 720
gctttattgc attttccacc atgccagagc tggctcagaa aatcaaaatg tattttgctt 780
tagcacccat agccactgtt aagcatgcaa aaagccccgg gaccaaattt ttgttgctgc 840
cagatatgat gatcaagga ttgtttggca aaaaagaatt tctgtatcag accagatttc 900
tcagacaact tgttatttac ctttgtggcc aggtgattct tgatcagatt tgtagtaata 960
tcatgttact tctgggtgga ttcaacacca acaatatgaa catgagccga gcaagtgtat 1020
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tgaattctgg tgaactccgg gcatttgact gggggagtga gacaaaaat ctggaaaaat 1140
gcaatcagcc aactcctgta aggtacagag tcagagatat gacggtcctt acagcaatgt 1200
ggacaggagg tcaggactgg ctttcaaate cagaagacgt gaaaatgctg ctctctgagg 1260
tgaccaacct catctaccat aagaatattc ctgaatgggc tcatgtggat ttcattctggg 1320
gtttggatgc tctcaccgt atgtacaatg aaatcatcca tctgatgcag caggaggaga 1380
ccat 1384

<210> 10
<211> 1915
<212> DNA
<213> Homo sapiens

<220>
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<222> (180)..(1046)

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cagtagcccg gcggcccagg gcaatccgac cacatttcac tctcaccgct gtaggaatcc 120
agatgcaggc caagtacagc agcacgaggg acatgctgga tgatgatggg gacaccacc 179
atg agc ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc 227
Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro
1 5 10 15
cgg cgc aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc 275
Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala
20 25 30

ctg acc ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala 35 40 45	323
ctg ggg ctt ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln 50 55 60	371
gac acc att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu 65 70 75 80	419
ttg caa tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln 85 90 95	467
cat gtg gct gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga ggc His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly 100 105 110	515
tat aca aga aac atg gtg cca gca tct gct tct tct gag agc ctc agg Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg 115 120 125	563
cag ctt cca cac atg ggg gaa agt gca gca gca cac agg tgc agc cct Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro 130 135 140	611
tgt aca gaa caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr 145 150 155 160	659
aaa gac agc aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu 165 170 175	707
aac tct acc atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala 180 185 190	755
gcg tct cag agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu 195 200 205	803
ttg cgc cct gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro 210 215 220	851
ttc act tct gaa ctg ttc cat att ata ata gat gtc acc agc cca aga Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg 225 230 235 240	899
agc aga gac tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp 245 250 255	947
tgc aaa gaa ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val 260 265 270	995
aag cca gag agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp 275 280 285	1043

tga ttgcacctct gcaactacaa atagcagagt gagccaggcg gtgccaaagc 1096
aagggctagt tgagacattg ggaaatggaa cataatcagg aaagactatc tctctgacta 1156
gtacaaaatg ggttctcgtg tttcctgttc aggatcacca gcatttctga gcttgggttt 1216
atgcacgtat ttaacagtca caagaagtct tatttacatg ccaccaacca acctcagaaa 1276
cccataatgt catctgcctt cttggcttag agataacttt tagctctctt tcttctcaat 1336
gtctaataatc acctccctgt tttcatgtct tccttacact tggtggaata agaaactttt 1396
tgaagtagag gaaatacatt gaggtaacat ccttttctct gacagtcaag tagtccatca 1456
gaaattggca gtcacttccc agattgtacc agcaaataca caaggaattc tttttgtttg 1516
tttcagttca tactagtccc ttcccaatcc atcagtaaag accccatctg ccttgtccat 1576
gccgtttccc aacaggggatg tcacttgata tgagaatctc aaatctcaat gccttataag 1636
cattccttcc tgtgtccatt aagactctga taattgtctc cctccatag gaatttctcc 1696
caggaaagaa atatatcccc atctccgttt catatcagaa ctaccgtccc cgatattccc 1756
ttcagagaga ttaaagacca gaaaaaaggg gggctttttt tttgcacctg taatagtttc 1816
cggtcctttt ttttttctt gaccctttt ttttcccttc cgggggtgga ggggttatta 1876
taattaaagg gaataccggg gaaaaaaaaa aaaaagggg 1915

<210> 11
<211> 288
<212> PRT
<213> Homo sapiens

<400> 11
Met Ser Leu His Ser Gln Ala Ser Ala Thr Arg His Pro Glu Pro
1 5 10 15
Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala
20 25 30
Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala
35 40 45
Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln
50 55 60
Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu
65 70 75 80
Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln
85 90 95
His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly
100 105 110

Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg
115 120 125

Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro
130 135 140

Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr
145 150 155 160

Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu
165 170 175

Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala
180 185 190

Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu
195 200 205

Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro
210 215 220

Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg
225 230 235 240

Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp
245 250 255

Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val
260 265 270

Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp
275 280 285

<210> 12
<211> 2420
<212> DNA
<213> Homo sapiens

<220>
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<222> (200)..(2395)

<220>
<221> misc_feature
<222> (2093)
<223> n = a, g, c or t

<220>
<221> misc_feature
<222> (2215)
<223> d = a or g or t; not c

<220>
<221> misc_feature
<222> (2332)
<223> b = c or g or t; not a

<220>
<221> misc_feature
<222> (2396)
<223> m = a or c

<220>
<221> misc_feature
<222> (632)
<223> Xaa = unknown or other

<220>
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<222> (672)
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<222> (711)
<223> Xaa = unknown or other

<400> 12
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aacggagaag ggggagagag ggggggtccag tctcccttgg ccgagcattt tttttttttg 120
gaagtcctag gactaatctc caggaccagc actcttctcc cagcccttag ggtcctgctc 180
ggccaaggcc ttccctgcc atg cga cct gtc agt gtc tgg cag tgg agc ccc 232
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro
1 5 10
tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tgc tgc ttg ggg tct ccg 280
Trp Gly Leu Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro
15 20 25
tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt cgg 328
Ser Pro Ser Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg
30 35 40
ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg gag 376
Phe Arg Leu Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu
45 50 55
ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc acg 424
Ile Gln Arg Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr
60 65 70 75
ctg cag gct gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag gcc 472
Leu Gln Ala Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala
80 85 90
aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc atc 520
Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile
95 100 105
tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act gaa 568
Trp Leu Asp Asn Leu Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu
110 115 120

tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag gat Cys Ala Ser Arg Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp 125 130 135	616
gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tcg gac tcc Ala Gly Val Ile Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser 140 145 150 155	664
aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga att Asn Val Ile Glu Val Glu His His Leu Gln Val Glu Glu Val Arg Ile 160 165 170	712
cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag ggg Arg Pro Ala Val Gly Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly 175 180 185	760
ctg gtg gaa gtc agg ctt cct gac ggc tgg tcg caa gtg tgc gac aaa Leu Val Glu Val Arg Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys 190 195 200	808
ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc ttc Gly Trp Ser Ala His Asn Ser His Val Val Cys Gly Met Leu Gly Phe 205 210 215	856
ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc caa Pro Ser Glu Lys Arg Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln 220 225 230 235	904
cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc acg Arg Gln Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr 240 245 250	952
gag gcc cac ctg tcc ctg tgt tcc ctg gag ttc tat cgt gcc aat gac Glu Ala His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp 255 260 265	1000
acc gcc agg tgc cct ggg ggg ggc cct gca gtg gtg agc tgt gtg cca Thr Ala Arg Cys Pro Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro 270 275 280	1048
ggc cct gtc tac gcg gca tcc agt ggc cag aag aag caa caa cag tcg Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser 285 290 295	1096
aag cct cag ggg gag gtc cgt gtc cgt cta aag ggc ggc gcc cac cct Lys Pro Gln Gly Glu Val Arg Val Arg Leu Lys Gly Gly Ala His Pro 300 305 310 315	1144
gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca gtc Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val 320 325 330	1192
tgt tac cgc aag tgg gac ctg cat gca gcc agc gtg gtg tgt cgg gag Cys Tyr Arg Lys Trp Asp Leu His Ala Ala Ser Val Val Cys Arg Glu 335 340 345	1240
ctg ggc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg ggg Leu Gly Phe Gly Ser Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly 350 355 360	1288
cag ggc atg ggt gct atc cac ctg agt gaa gtt cgc tgc tct gga cag Gln Gly Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln 365 370 375	1336

gag ctc tcc ctc tgg aag tgc ccc cac aag aac atc aca gct gag gat Glu Leu Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp 380 385 390 395	1384
tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac act Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr 400 405 410	1432
ggg gca gag acc agg gtc atc cat tct gtg tca cta cag atc cga ctc Gly Ala Glu Thr Arg Val Ile His Ser Val Ser Leu Gln Ile Arg Leu 415 420 425	1480
agt ggg ggc cgc agc caa cat gag ggg cga gtc gag gtg caa ata ggg Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val Gln Ile Gly 430 435 440	1528
gga cct ggg ccc ctt cgc tgg ggc ctc atc tgt ggg gat gac tgg ggg Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly 445 450 455	1576
acc ctg gag gcc atg gtg gcc tgt agg caa ctg ggt ctg ggc tac gcc Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu Gly Tyr Ala 460 465 470 475	1624
aac cac ggc ctg cag gag acc tgg tac tgg gac tct ggg aat ata aca Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr 480 485 490	1672
gag gtg gtg atg agt gga gtg cgc tgc aca ggg act gag ctg tcc ctg Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu Leu Ser Leu 495 500 505	1720
gat cag tgt gcc cat cat ggc acc cac atc acc tgc aag agg aca ggg Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys Arg Thr Gly 510 515 520	1768
acc cgc ttc act gct gga gtc atc tgt tct gag gca tca gat ctg ttg Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Ala Ser Asp Leu Leu 525 530 535	1816
ctg cac tca gca ctg gtg cag gag acc gcc tac atc gaa gac cgg ccc Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro 540 545 550 555	1864
ctg cat atg ttg tac tgt gct gcg gaa gag aac tgc ctg gcc agc tca Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser 560 565 570	1912
gcc cgc tca gcc aac tgg ccc tat ggt cac cgg cgt ctg ctc cga ttc Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg Leu Leu Arg Phe 575 580 585	1960
tgc tcc cag atc cac aac ctg gga cga gct gac ttc agg ccc aag gct Cys Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala 590 595 600	2008
ggg cgc cac tcc tgg gtg tgg cac gag tgc cat ggg cat tac cac agc Gly Arg His Ser Trp Val Trp His Glu Cys His Gly His Tyr His Ser 605 610 615	2056
acg gac ttc ttc act cac tat gat atc ctc acc cca nat ggc acc aag Thr Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro Xaa Gly Thr Lys 620 625 630 635	2104

gtg gct gag ggc cac aaa gct agt ttc tgt ctc gaa gac act gag tgt	2152
Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys	
640 645 650	
cag gag gat gtc tcc aag cgg tat gag tgt gcc aac ttt gga gag caa	2200
Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln	
655 660 665	
ggc atc act gtg ggd tgc tgg gat ctc tac cgg cat gac att gac tgt	2248
Gly Ile Thr Val Xaa Cys Trp Asp Leu Tyr Arg His Asp Ile Asp Cys	
670 675 680	
cag tgg att gac atc acg gat gtg aag cca gga aac tac att ctc cag	2296
Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln	
685 690 695	
gtt gtc atc aac cca aac ttt gaa gta gca gag agb gac ttt acc aac	2344
Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Xaa Asp Phe Thr Asn	
700 705 710 715	
aat gca atg aaa tgt aac tgc aaa tat gat gga cat aga atc tgg gtg	2392
Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His Arg Ile Trp Val	
720 725 730	
cac macttgccac attggtgatg ccttc	2420
His	

<210> 13
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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (632)
 <223> Xaa = unknown or other

<220>
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<400> 13
 Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu
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Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
 20 25 30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
 35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
65 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
100 105 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
115 120 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
130 135 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
145 150 155 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
165 170 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
180 185 190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
195 200 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
210 215 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser
225 230 235 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser
245 250 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
260 265 270

Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala
275 280 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu
290 295 300

Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val
305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Tyr Arg Lys Trp
325 330 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser
340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala
355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp
370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln
385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
405 410 415

Val Ile His Ser Val Ser Leu Gln Ile Arg Leu Ser Gly Gly Arg Ser
420 425 430

Gln His Glu Gly Arg Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu
435 440 445

Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met
450 455 460

Val Ala Cys Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln
465 470 475 480

Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser
485 490 495

Gly Val Arg Cys Thr Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His
500 505 510

His Gly Thr His Ile Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala
515 520 525

Gly Val Ile Cys Ser Glu Ala Ser Asp Leu Leu Leu His Ser Ala Leu
530 535 540

Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr
545 550 555 560

Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn
565 570 575

Trp Pro Tyr Gly His Arg Arg Leu Leu Arg Phe Cys Ser Gln Ile His
580 585 590

Asn Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp
595 600 605

Val Trp His Glu Cys His Gly His Tyr His Ser Thr Asp Phe Phe Thr
610 615 620

His Tyr Asp Ile Leu Thr Pro Xaa Gly Thr Lys Val Ala Glu Gly His
625 630 635 640

Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser
645 650 655

Lys Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Xaa
660 665 670

Cys Trp Asp Leu Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile
675 680 685

Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro
690 695 700

Asn Phe Glu Val Ala Glu Xaa Asp Phe Thr Asn Asn Ala Met Lys Cys
705 710 715 720

Asn Cys Lys Tyr Asp Gly His Arg Ile Trp Val His
725 730

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<222> (149)..(2065)

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tccctccacc ttccacatcc tgctccaggc aggagaaggc tgactggctg gactcattga 120
gctgaagaat ttccagtgc atttgtaa atg acg ccg ctc gat tcc agg ctc 172
Met Thr Pro Leu Asp Ser Arg Leu
1 5

caa gcg gcc cct gcc gcc gcc gcc gcc gcc ggg ccg aag gtg ccg ccg Gln Ala Ala Pro Ala Ala Ala Ala Ala Ala Gly Pro Lys Val Pro Pro 10 15 20	220
agc agt ctc cag cgc agg ctt cct tac cgg gcg acc aca atg tcc gag Ser Ser Leu Gln Arg Arg Leu Pro Tyr Arg Ala Thr Thr Met Ser Glu 25 30 35 40	268
ttt ctc ctc gcc tta ctc act ctc tcg gga tta ttg ccg att gcc agg Phe Leu Leu Ala Leu Leu Thr Leu Ser Gly Leu Leu Pro Ile Ala Arg 45 50 55	316
gtg ctg acc gtg gga gcc gac cga gat cag cag ttg tgt gat cct ggt Val Leu Thr Val Gly Ala Asp Arg Asp Gln Gln Leu Cys Asp Pro Gly 60 65 70	364
gaa ttt ctt tgc cac gat cac gtg act tgt gtc tcc cag agc tgg ctg Glu Phe Leu Cys His Asp His Val Thr Cys Val Ser Gln Ser Trp Leu 75 80 85	412
tgt gat ggg gac cct gac tgc cct gat gat tca gac gag tct tta gat Cys Asp Gly Asp Pro Asp Cys Pro Asp Asp Ser Asp Glu Ser Leu Asp 90 95 100	460
acc tgt ccc gag gag gta gaa atc aag tgc ccc ttg aat cac att gct Thr Cys Pro Glu Glu Val Glu Ile Lys Cys Pro Leu Asn His Ile Ala 105 110 115 120	508
tgc ctt ggc acc aac aaa tgt gtt cat tta tcc cag ctg tgc aat ggt Cys Leu Gly Thr Asn Lys Cys Val His Leu Ser Gln Leu Cys Asn Gly 125 130 135	556
gtc ttg gac tgc cca gat ggg tat gac gaa gga gta cat tgt cag gaa Val Leu Asp Cys Pro Asp Gly Tyr Asp Glu Gly Val His Cys Gln Glu 140 145 150	604
ctg tta tcc aat tgc caa cag ctg aat tgt cag tat aaa tgt aca atg Leu Leu Ser Asn Cys Gln Gln Leu Asn Cys Gln Tyr Lys Cys Thr Met 155 160 165	652
gtc aga aat agt aca aga tgt tac tgt gag gat gga ttc gaa ata aca Val Arg Asn Ser Thr Arg Cys Tyr Cys Glu Asp Gly Phe Glu Ile Thr 170 175 180	700
gaa gat ggg aga agc tgt aaa gat caa gat gaa tgt gct gtt tat ggt Glu Asp Gly Arg Ser Cys Lys Asp Gln Asp Glu Cys Ala Val Tyr Gly 185 190 195 200	748
aca ggc agc cag acc tgc aga aac aca cat gga tcc tac act tgc agt Thr Gly Ser Gln Thr Cys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser 205 210 215	796
tgt gtg gaa ggc tac cta atg cag cca gac agc aga tct tgc aag gct Cys Val Glu Gly Tyr Leu Met Gln Pro Asp Ser Arg Ser Cys Lys Ala 220 225 230	844
aaa att gaa cct aca gat aga cca cgt ata cta tta att gca aat ttt Lys Ile Glu Pro Thr Asp Arg Pro Arg Ile Leu Leu Ile Ala Asn Phe 235 240 245	892
gaa tca att gag gtt ttc tat ctt aat gga agt aaa att gca act cta Glu Ser Ile Glu Val Phe Tyr Leu Asn Gly Ser Lys Ile Ala Thr Leu 250 255 260	940

agc tca gtc aat gga aat gaa att cat act ctg gat ttt att tat aat	988
Ser Ser Val Asn Gly Asn Glu Ile His Thr Leu Asp Phe Ile Tyr Asn	
265 270 275 280	
gaa gat gtg att tgt tgg att gaa tca aga gaa tct tca aat caa ctc	1036
Glu Asp Val Ile Cys Trp Ile Glu Ser Arg Glu Ser Ser Asn Gln Leu	
285 290 295	
aaa tgt atc cag ata aca aaa gca gga gga tta aca gat gaa tgg aca	1084
Lys Cys Ile Gln Ile Thr Lys Ala Gly Gly Leu Thr Asp Glu Trp Thr	
300 305 310	
atc aat att ctt caa tcc ttc cac aat gtg caa caa atg gcg att gac	1132
Ile Asn Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp	
315 320 325	
tgg ctc act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc	1180
Trp Leu Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile	
330 335 340	
ttt gtt tgt aat tcc aac ggt tct gta tgt gtc acc ctg att gat ctg	1228
Phe Val Cys Asn Ser Asn Gly Ser Val Cys Val Thr Leu Ile Asp Leu	
345 350 355 360	
gag ctt cac aat cct aaa gca ata gca gta gat cca ata gca gga aaa	1276
Glu Leu His Asn Pro Lys Ala Ile Ala Val Asp Pro Ile Ala Gly Lys	
365 370 375	
ctt ttc ttt act gac tac ggg aat gtc gcc aaa gtg gag aga tgt gac	1324
Leu Phe Phe Thr Asp Tyr Gly Asn Val Ala Lys Val Glu Arg Cys Asp	
380 385 390	
atg gat ggg atg aac cga aca agg ata att gat tca aag aca gag cag	1372
Met Asp Gly Met Asn Arg Thr Arg Ile Ile Asp Ser Lys Thr Glu Gln	
395 400 405	
cca gct gca ctg gca cta gac cta gtc aac aaa ttg gtt tac tgg gta	1420
Pro Ala Ala Leu Ala Leu Asp Leu Val Asn Lys Leu Val Tyr Trp Val	
410 415 420	
gat ctt tac ttg gac tat gtg gga gta gtg gac tat caa gga aaa aat	1468
Asp Leu Tyr Leu Asp Tyr Val Gly Val Val Asp Tyr Gln Gly Lys Asn	
425 430 435 440	
aga cac act gtc att caa ggc aga caa gtc aga cat ctt tat ggt ata	1516
Arg His Thr Val Ile Gln Gly Arg Gln Val Arg His Leu Tyr Gly Ile	
445 450 455	
act gtg ttt gaa gat tat ttg tat gca acc aat tct gat aac tac aat	1564
Thr Val Phe Glu Asp Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Tyr Asn	
460 465 470	
atc gta agg ata aac cga ttt aat ggg act gat att cac tca tta att	1612
Ile Val Arg Ile Asn Arg Phe Asn Gly Thr Asp Ile His Ser Leu Ile	
475 480 485	
aaa att gag aat gct tgg gga atc cga att tat caa aaa aga act caa	1660
Lys Ile Glu Asn Ala Trp Gly Ile Arg Ile Tyr Gln Lys Arg Thr Gln	
490 495 500	
cca aca gtc aga agc cat gca tgt gaa gtc gat cca tat gga atg cca	1708
Pro Thr Val Arg Ser His Ala Cys Glu Val Asp Pro Tyr Gly Met Pro	
505 510 515 520	

ggg ggc tgt tca cac atc tgt cta ctc agc agc agt tac aaa act cgg 1756
Gly Gly Cys Ser His Ile Cys Leu Leu Ser Ser Ser Tyr Lys Thr Arg
525 530 535

act tgt cgc tgc agg act ggc ttc aac ttg gga agt gat ggc agg tca 1804
Thr Cys Arg Cys Arg Thr Gly Phe Asn Leu Gly Ser Asp Gly Arg Ser
540 545 550

tgc aaa aga cca aag aat gag ttg ttc ctc ttt tat ggg aaa gga cgc 1852
Cys Lys Arg Pro Lys Asn Glu Leu Phe Leu Phe Tyr Gly Lys Gly Arg
555 560 565

cca gga att gtt aga gga atg gac ttg aat acc aag ata gct gat gaa 1900
Pro Gly Ile Val Arg Gly Met Asp Leu Asn Thr Lys Ile Ala Asp Glu
570 575 580

tac atg atc ccc ata gaa aat ctg gta aac cct cgt gct tta gac ttt 1948
Tyr Met Ile Pro Ile Glu Asn Leu Val Asn Pro Arg Ala Leu Asp Phe
585 590 595 600

cac gca gaa acc aat tac atc tac ttt gct gac acc acc agt ttc cta 1996
His Ala Glu Thr Asn Tyr Ile Tyr Phe Ala Asp Thr Thr Ser Phe Leu
605 610 615

att ggc cgg cag aag ata gat ggc aca gag aga gaa acc atc ctg aaa 2044
Ile Gly Arg Gln Lys Ile Asp Gly Thr Glu Arg Glu Thr Ile Leu Lys
620 625 630

gat gat ctg gat aat gta gag g 2066
Asp Asp Leu Asp Asn Val Glu
635

<210> 15
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Tyr Arg Ala Thr Thr Met Ser Glu Phe Leu Leu Ala Leu Leu Thr Leu
35 40 45

Ser Gly Leu Leu Pro Ile Ala Arg Val Leu Thr Val Gly Ala Asp Arg
50 55 60

Asp Gln Gln Leu Cys Asp Pro Gly Glu Phe Leu Cys His Asp His Val
65 70 75 80

Thr Cys Val Ser Gln Ser Trp Leu Cys Asp Gly Asp Pro Asp Cys Pro
85 90 95

Asp Asp Ser Asp Glu Ser Leu Asp Thr Cys Pro Glu Glu Val Glu Ile
100 105 110

Lys Cys Pro Leu Asn His Ile Ala Cys Leu Gly Thr Asn Lys Cys Val
115 120 125

His Leu Ser Gln Leu Cys Asn Gly Val Leu Asp Cys Pro Asp Gly Tyr
130 135 140

Asp Glu Gly Val His Cys Gln Glu Leu Leu Ser Asn Cys Gln Gln Leu
145 150 155 160

Asn Cys Gln Tyr Lys Cys Thr Met Val Arg Asn Ser Thr Arg Cys Tyr
165 170 175

Cys Glu Asp Gly Phe Glu Ile Thr Glu Asp Gly Arg Ser Cys Lys Asp
180 185 190

Gln Asp Glu Cys Ala Val Tyr Gly Thr Gly Ser Gln Thr Cys Arg Asn
195 200 205

Thr His Gly Ser Tyr Thr Cys Ser Cys Val Glu Gly Tyr Leu Met Gln
210 215 220

Pro Asp Ser Arg Ser Cys Lys Ala Lys Ile Glu Pro Thr Asp Arg Pro
225 230 235 240

Arg Ile Leu Leu Ile Ala Asn Phe Glu Ser Ile Glu Val Phe Tyr Leu
245 250 255

Asn Gly Ser Lys Ile Ala Thr Leu Ser Ser Val Asn Gly Asn Glu Ile
260 265 270

His Thr Leu Asp Phe Ile Tyr Asn Glu Asp Val Ile Cys Trp Ile Glu
275 280 285

Ser Arg Glu Ser Ser Asn Gln Leu Lys Cys Ile Gln Ile Thr Lys Ala
290 295 300

Gly Gly Leu Thr Asp Glu Trp Thr Ile Asn Ile Leu Gln Ser Phe His
305 310 315 320

Asn Val Gln Gln Met Ala Ile Asp Trp Leu Thr Arg Asn Leu Tyr Phe
325 330 335

Val Asp His Val Gly Asp Arg Ile Phe Val Cys Asn Ser Asn Gly Ser
340 345 350

Val Cys Val Thr Leu Ile Asp Leu Glu Leu His Asn Pro Lys Ala Ile
355 360 365

Ala Val Asp Pro Ile Ala Gly Lys Leu Phe Phe Thr Asp Tyr Gly Asn
370 375 380

Val Ala Lys Val Glu Arg Cys Asp Met Asp Gly Met Asn Arg Thr Arg
385 390 395 400

Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala Ala Leu Ala Leu Asp Leu
405 410 415

Val Asn Lys Leu Val Tyr Trp Val Asp Leu Tyr Leu Asp Tyr Val Gly
420 425 430

Val Val Asp Tyr Gln Gly Lys Asn Arg His Thr Val Ile Gln Gly Arg
435 440 445

Gln Val Arg His Leu Tyr Gly Ile Thr Val Phe Glu Asp Tyr Leu Tyr
450 455 460

Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val Arg Ile Asn Arg Phe Asn
465 470 475 480

Gly Thr Asp Ile His Ser Leu Ile Lys Ile Glu Asn Ala Trp Gly Ile
485 490 495

Arg Ile Tyr Gln Lys Arg Thr Gln Pro Thr Val Arg Ser His Ala Cys
500 505 510

Glu Val Asp Pro Tyr Gly Met Pro Gly Gly Cys Ser His Ile Cys Leu
515 520 525

Leu Ser Ser Ser Tyr Lys Thr Arg Thr Cys Arg Cys Arg Thr Gly Phe
530 535 540

Asn Leu Gly Ser Asp Gly Arg Ser Cys Lys Arg Pro Lys Asn Glu Leu
545 550 555 560

Phe Leu Phe Tyr Gly Lys Gly Arg Pro Gly Ile Val Arg Gly Met Asp
565 570 575

Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met Ile Pro Ile Glu Asn Leu
580 585 590

Val Asn Pro Arg Ala Leu Asp Phe His Ala Glu Thr Asn Tyr Ile Tyr
595 600 605

Phe Ala Asp Thr Thr Ser Phe Leu Ile Gly Arg Gln Lys Ile Asp Gly
610 615 620

Thr Glu Arg Glu Thr Ile Leu Lys Asp Asp Leu Asp Asn Val Glu
625 630 635

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atctggaacc aaaatcactt cccggaattg accaactggg agactcgcct agaggggaag 180
cattgtgtcc tagttgaggc taacagtcag tatccagcct caacattcag cagaggcccc 240
agatcagcgt ctgagccagg ccaacaatga ccaaggagg atg gga tcc tgg gtg 294
Met Gly Ser Trp Val
1 5
cag ctc atc aca agc gtc ggg gtg cag caa aac cat cca ggc tgg aca 342
Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn His Pro Gly Trp Thr
10 15 20
gtg gct gga cag ttc caa gaa aag aaa cgc ttc act gaa gaa gtc att 390
Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe Thr Glu Glu Val Ile
25 30 35
gaa tac ttc cag aag aaa gtt agc cca gtg cat ctg aaa atc ctg ctg 438
Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His Leu Lys Ile Leu Leu
40 45 50
act agc gat gaa gcc tgg aag aga ttc gtg cgt gtg gct gaa ttg ccc 486
Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg Val Ala Glu Leu Pro
55 60 65
agg gaa gaa gca gat gct ctc tat gaa gct ctg aag aat ctt aca cca 534
Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu Lys Asn Leu Thr Pro
70 75 80 85
tat gtg gct att gag gac aaa gac atg cag caa aaa gaa cag cag ttt 582
Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln Lys Glu Gln Gln Phe
90 95 100
agg gag tgg ttt ttg aaa gag ttt cct caa atc aga tgg aag att cag 630
Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile Arg Trp Lys Ile Gln
105 110 115
gag tcc ata gaa agg ctt cgt gtc att gca aat gag att gaa aag gtc 678
Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn Glu Ile Glu Lys Val
120 125 130

cac aga ggc tgc gtc atc gcc aat gtg gtg tct ggc tcc act ggc atc His Arg Gly Cys Val Ile Ala Asn Val Val Ser Gly Ser Thr Gly Ile 135 140 145	726
ctg tct gtc att ggc gtt atg ttg gca cca ttt aca gca ggg ctg agc Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe Thr Ala Gly Leu Ser 150 155 160 165	774
ctg agc att act gca gct ggg gta ggg ctg gga ata gca tct gcc acg Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly Ile Ala Ser Ala Thr 170 175 180	822
gct ggg atc gcc tcc agc atc gtg gag aac aca tac aca agg tca gca Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr Tyr Thr Arg Ser Ala 185 190 195	870
gaa ctc aca gcc agc agg ctg act gca acc agc act gac caa ttg gag Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser Thr Asp Gln Leu Glu 200 205 210	918
gca tta agg gac att ctg cgt gac atc aca ccc aat gtg ctt tct ttt Ala Leu Arg Asp Ile Leu Arg Asp Ile Thr Pro Asn Val Leu Ser Phe 215 220 225	966
gca ctt gat ttt gac gaa gcc aca aaa atg att gcg aat gat gtc cat Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile Ala Asn Asp Val His 230 235 240 245	1014
aca ctc agg aga tct aaa gcc act gtt gga cgc cct ttg att gct tgg Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg Pro Leu Ile Ala Trp 250 255 260	1062
cga tat gta cct ata aat gtt gtt gag aca ctg aga aca cgt ggg gcc Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu Arg Thr Arg Gly Ala 265 270 275	1110
ccc acc cgg ata gtg aga aaa gta gcc cgg aac ctg ggc aag gcc act Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn Leu Gly Lys Ala Thr 280 285 290	1158
tca ggt gtc ctt gtt gtg ctg gat gta gtc aac ctt gtg caa gac tca Ser Gly Val Leu Val Val Leu Asp Val Val Asn Leu Val Gln Asp Ser 295 300 305	1206
ctg gac ttg cac aag ggg gca aaa tcc gag tct gct gag tcg ctg agg Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser Ala Glu Ser Leu Arg 310 315 320 325	1254
cag tgg gct cag gag ctg gag gag aat ctc aat gag ctc acc cat atc Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn Glu Leu Thr His Ile 330 335 340	1302
cat cag agt cta aaa gca ggc taggcccaat His Gln Ser Leu Lys Ala Gly 345	1333

<210> 17
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 <213> Homo sapiens

<400> 17

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His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe
20 25 30

Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
35 40 45

Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
50 55 60

Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
65 70 75 80

Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln
85 90 95

Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile
100 105 110

Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn
115 120 125

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser
130 135 140

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe
145 150 155 160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly
165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr
180 185 190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser
195 200 205

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu Arg Asp Ile Thr Pro
210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile
225 230 235 240

Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg
245 250 255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu
260 265 270

Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn
275 280 285

Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn
290 295 300

Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser
305 310 315 320

Ala Glu Ser Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn
325 330 335

Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly
340 345

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atctggtgcc agctggtgga acagtgggtg atg gcg tcc ctg ctg caa gac cag 174
Met Ala Ser Leu Leu Gln Asp Gln
1 5
ctg acc act gat cag gac ttg ctg ctg atg cag gaa ggc atg ccg atg 222
Leu Thr Thr Asp Gln Asp Leu Leu Leu Met Gln Glu Gly Met Pro Met
10 15 20
cgc aag gtg agg tcc aaa agc tgg aag aag cta aga tac ttc aga ctt 270
Arg Lys Val Arg Ser Lys Ser Trp Lys Lys Leu Arg Tyr Phe Arg Leu
25 30 35 40
cag aat gac ggc atg aca gtc tgg cat gca cgg cag gcc agg ggc agt 318
Gln Asn Asp Gly Met Thr Val Trp His Ala Arg Gln Ala Arg Gly Ser
45 50 55
gcc aag ccc agc ttc tca atc tct gat gtg gag aca ata cgt aat ggc 366
Ala Lys Pro Ser Phe Ser Ile Ser Asp Val Glu Thr Ile Arg Asn Gly
60 65 70
cat gat tcc gag ttg ctg cgt agc ctg gca gag gag ctc ccc ctg gag 414
His Asp Ser Glu Leu Leu Arg Ser Leu Ala Glu Glu Leu Pro Leu Glu
75 80 85

cag ggc ttc acc att gtc ttc cat ggc cgc cgc tcc aac ctg gac ctg Gln Gly Phe Thr Ile Val Phe His Gly Arg Arg Ser Asn Leu Asp Leu 90 95 100	462
atg gcc aac agt gtt gag gag gcc cag ata tgg atg cga ggg ctc cag Met Ala Asn Ser Val Glu Glu Ala Gln Ile Trp Met Arg Gly Leu Gln 105 110 115 120	510
ctg ttg gtg gat ctt gtc acc agc atg gac cat cag gag cgc ctg gac Leu Leu Val Asp Leu Val Thr Ser Met Asp His Gln Glu Arg Leu Asp 125 130 135	558
caa tgg ctg agc gat tgg ttt caa cgt gga gac aaa aat cag gat ggt Gln Trp Leu Ser Asp Trp Phe Gln Arg Gly Asp Lys Asn Gln Asp Gly 140 145 150	606
aag atg agt ttc caa gaa gtt cag cgg tta ttg cac cta atg aat gtg Lys Met Ser Phe Gln Glu Val Gln Arg Leu Leu His Leu Met Asn Val 155 160 165	654
gaa atg gac caa gaa tat gcc ttc agt ctt ttt cag gca gca gac acg Glu Met Asp Gln Glu Tyr Ala Phe Ser Leu Phe Gln Ala Ala Asp Thr 170 175 180	702
tcc cag tct gga acc ctg gaa gga gaa gaa ttc gta cag ttc tat aag Ser Gln Ser Gly Thr Leu Glu Gly Glu Glu Phe Val Gln Phe Tyr Lys 185 190 195 200	750
gca ttg act aaa cgt gct gag gtg cag gaa ctg ttt gaa agt ttt tca Ala Leu Thr Lys Arg Ala Glu Val Gln Glu Leu Phe Glu Ser Phe Ser 205 210 215	798
gct gat ggg cag aag ctg act ctg ctg gaa ttt ttg gat ttc ctc caa Ala Asp Gly Gln Lys Leu Thr Leu Glu Phe Leu Asp Phe Leu Gln 220 225 230	846
gag gag cag aag gag aga gac tgc acc tct gag ctt gct ctg gaa ctc Glu Glu Gln Lys Glu Arg Asp Cys Thr Ser Glu Leu Ala Leu Glu Leu 235 240 245	894
att gac cgc tat gaa cct tca gac agt ggc aaa ctg cgg cat gtg ctg Ile Asp Arg Tyr Glu Pro Ser Asp Ser Gly Lys Leu Arg His Val Leu 250 255 260	942
agt atg gat ggc ttc ctc agc tac ctc tgc tct aag gat gga gac atc Ser Met Asp Gly Phe Leu Ser Tyr Leu Cys Ser Lys Asp Gly Asp Ile 265 270 275 280	990
ttc aac cca gcc tgc ctc ccc atc tat cag gat atg act caa ccc ctg Phe Asn Pro Ala Cys Leu Pro Ile Tyr Gln Asp Met Thr Gln Pro Leu 285 290 295	1038
aac cac tac ttc atc tgc tct tct cat aac acc tac cta gtg ggg gac Asn His Tyr Phe Ile Cys Ser Ser His Asn Thr Tyr Leu Val Gly Asp 300 305 310	1086
cag ctt tgc ggc cag agc agc gtc gag gga tat ata cgg tgc agt ggt Gln Leu Cys Gly Gln Ser Ser Val Glu Gly Tyr Ile Arg Cys Ser Gly 315 320 325	1134
ggt aga gaa ggg gtc caa ctc atg aga ggg acc atg tagaaaagtg Gly Arg Glu Gly Val Gln Leu Met Arg Gly Thr Met 330 335 340	1180

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aggggagctg tcagtgtcta acagattggg acagtgttgt gggggtttag gggctgagga 1240
gccctggata ccagagacac ttggaggaga tattgaagac tggtagggaga atggtaatga 1300
aaccctatgg gtcaatggaa cttctctttc acaagctatg aaactctcct ggaactcaga 1360
ggccctgaca gatttatatt taacaaatta ataaacagat tggtaaatgg aaggcaatag 1420
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ctttacttgg                                     1490

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<212> PRT
<213> Homo sapiens

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Leu Met Gln Glu Gly Met Pro Met Arg Lys Val Arg Ser Lys Ser Trp
          20          25          30

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```

Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn Asp Gly Met Thr Val Trp
35          40          45

```

```

His Ala Arg Gln Ala Arg Gly Ser Ala Lys Pro Ser Phe Ser Ile Ser
50          55          60

```

```

Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser Glu Leu Leu Arg Ser
65          70          75          80

```

```

Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe Thr Ile Val Phe His
85          90          95

```

```

Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn Ser Val Glu Glu Ala
100          105          110

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Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val Asp Leu Val Thr Ser
115          120          125

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```

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln
130          135          140

```

```

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln
145          150          155          160

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```

Arg Leu Leu His Leu Met Asn Val Glu Met Asp Gln Glu Tyr Ala Phe
165          170          175

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Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly
180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val
195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu
210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Glu Gln Lys Glu Arg Asp Cys
225 230 235 240

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp
245 250 255

Ser Gly Lys Leu Arg His Val Leu Ser Met Asp Gly Phe Leu Ser Tyr
260 265 270

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile
275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser
290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val
305 310 315 320

Glu Gly Tyr Ile Arg Cys Ser Gly Gly Arg Glu Gly Val Gln Leu Met
325 330 335

Arg Gly Thr Met
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<213> Homo sapiens

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<222> (189)..(1415)

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gaaaaaataa atgcagatgt tggaccatgt tggaaacctt gtcaagacag tggattgtct 180
cacacaga atg gaa atg tgg ctt ctg att ctg gtg gcg tat atg ttc cag 230
Met Glu Met Trp Leu Leu Ile Leu Val Ala Tyr Met Phe Gln
1 5 10

aga aat gtg aat tca gta cat atg cca act aaa gct gtg gac cca gaa	278
Arg Asn Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu	
15 20 25 30	
gca ttc atg aat att agt gaa atc atc caa cat caa ggc tat ccc tgt	326
Ala Phe Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys	
35 40 45	
gag gaa tat gaa gtc gca act gaa gat ggg tat atc ctt tct gtt aac	374
Glu Glu Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn	
50 55 60	
agg att cct cga ggc cta gtg caa cct aag aag aca ggt tcc agg cct	422
Arg Ile Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro	
65 70 75	
gtg gtg tta ctg cag cat ggc cta gtt gga ggt gct agc aac tgg att	470
Val Val Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile	
80 85 90	
tcc aac ctg ccc aac aat agc ctg ggc ttc att ctg gca gat gct ggt	518
Ser Asn Leu Pro Asn Asn Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly	
95 100 105 110	
ttt gac gtg tgg atg ggg aac agc agg gga aac gcc tgg tct cga aaa	566
Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys	
115 120 125	
cac aag aca ctc tcc ata gac caa gat gag ttc tgg gct ttc agt tat	614
His Lys Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr	
130 135 140	
gat gag atg gct agg ttt gac ctt cct gca gtg ata aac ttt att ttg	662
Asp Glu Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu	
145 150 155	
cag aaa acg ggc cag gaa aag atc tat tat gtc ggc tat tca cag ggc	710
Gln Lys Thr Gly Gln Glu Lys Ile Tyr Tyr Val Gly Tyr Ser Gln Gly	
160 165 170	
acc acc atg ggc ttt att gca ttt tcc acc atg cca gag ctg gct cag	758
Thr Thr Met Gly Phe Ile Ala Phe Ser Thr Met Pro Glu Leu Ala Gln	
175 180 185 190	
aaa atc aaa atg tat ttt gct tta gca ccc ata gcc act gtt aag cat	806
Lys Ile Lys Met Tyr Phe Ala Leu Ala Pro Ile Ala Thr Val Lys His	
195 200 205	
gca aaa agc ccc ggg acc aaa ttt ttg ttg ctg cca gat atg atg atc	854
Ala Lys Ser Pro Gly Thr Lys Phe Leu Leu Leu Pro Asp Met Met Ile	
210 215 220	
aag gga ttg ttt ggc aaa aaa gaa ttt ctg tat cag acc aga ttt ctc	902
Lys Gly Leu Phe Gly Lys Lys Glu Phe Leu Tyr Gln Thr Arg Phe Leu	
225 230 235	
aga caa ctt gtt att tac ctt tgt ggc cag gtg att ctt gat cag att	950
Arg Gln Leu Val Ile Tyr Leu Cys Gly Gln Val Ile Leu Asp Gln Ile	
240 245 250	
tgt agt aat atc atg tta ctt ctg ggt gga ttc aac acc aac aat atg	998
Cys Ser Asn Ile Met Leu Leu Leu Gly Gly Phe Asn Thr Asn Asn Met	
255 260 265 270	

aac atg agc cga gca agt gta tat gct gcc cac act ctt gct gga aca Asn Met Ser Arg Ala Ser Val Tyr Ala Ala His Thr Leu Ala Gly Thr 275 280 285	1046
tct gtg caa aat att cta cac tgg agc cag gca gtg aat tct ggt gaa Ser Val Gln Asn Ile Leu His Trp Ser Gln Ala Val Asn Ser Gly Glu 290 295 300	1094
ctc cgg gca ttt gac tgg ggg agt gag acc aaa aat ctg gaa aaa tgc Leu Arg Ala Phe Asp Trp Gly Ser Glu Thr Lys Asn Leu Glu Lys Cys 305 310 315	1142
aat cag cca act cct gta agg tac aga gtc aga gat atg acg gtc cct Asn Gln Pro Thr Pro Val Arg Tyr Arg Val Arg Asp Met Thr Val Pro 320 325 330	1190
aca gca atg tgg aca gga ggt cag gac tgg ctt tca aat cca gaa gac Thr Ala Met Trp Thr Gly Gly Gln Asp Trp Leu Ser Asn Pro Glu Asp 335 340 345 350	1238
gtg aaa atg ctg ctc tct gag gtg acc aac ctc atc tac cat aag aat Val Lys Met Leu Leu Ser Glu Val Thr Asn Leu Ile Tyr His Lys Asn 355 360 365	1286
att cct gaa tgg gct cat gtg gat ttc atc tgg ggt ttg gat gct cct Ile Pro Glu Trp Ala His Val Asp Phe Ile Trp Gly Leu Asp Ala Pro 370 375 380	1334
cac cgt atg tac aat gaa atc atc cat ctg atg cag cag gag gag acc His Arg Met Tyr Asn Glu Ile Ile His Leu Met Gln Gln Glu Glu Thr 385 390 395	1382
aac ctt tcc cag gga cgg tgt gag gcc gta ttg tgaagcatct gacactgacg Asn Leu Ser Gln Gly Arg Cys Glu Ala Val Leu 400 405	1435
atcttaggac aacctcctga gggatggggc taggacccat gaaggcagaa ttatggagag	1495
cagagaccta gtatacattt ttcagattcc ctgcacttgg cactaaatcc gacacttaca	1555
tttacatttt ttttctgtaa attaaagtac ttattaggta aatagagggt ttgtatgcta	1615
ttatatattc taccatcttg aagggtaggt ttacctgat agccagaaaa tatctagaca	1675
ttctctatat cattcaggta aatctcttta aaacacctat tgttttttct ataagccata	1735
tttttggagc actaaagtaa aatggcaaat tgggacagat attgagggtc ggagtctgtg	1795
gattattggt gactttgaca aaataagcta gacattttca ccttggtgcc acagagacat	1855
aacactacct caggaagctg agctgcttta aggacaacaa caacaaaatc agtggttacag	1915
tatggatgaa atctatgtta agcattctca gaataaggcc aagttttata gttgcatctc	1975
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<212> PRT	
<213> Homo sapiens	

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Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu Ala Phe
20 25 30

Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys Glu Glu
35 40 45

Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn Arg Ile
50 55 60

Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro Val Val
65 70 75 80

Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile Ser Asn
85 90 95

Leu Pro Asn Asn Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly Phe Asp
100 105 110

Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys His Lys
115 120 125

Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu
130 135 140

Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu Gln Lys
145 150 155 160

Thr Gly Gln Glu Lys Ile Tyr Tyr Val Gly Tyr Ser Gln Gly Thr Thr
165 170 175

Met Gly Phe Ile Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Lys Ile
180 185 190

Lys Met Tyr Phe Ala Leu Ala Pro Ile Ala Thr Val Lys His Ala Lys
195 200 205

Ser Pro Gly Thr Lys Phe Leu Leu Leu Pro Asp Met Met Ile Lys Gly
210 215 220

Leu Phe Gly Lys Lys Glu Phe Leu Tyr Gln Thr Arg Phe Leu Arg Gln
225 230 235 240

Leu Val Ile Tyr Leu Cys Gly Gln Val Ile Leu Asp Gln Ile Cys Ser
245 250 255

Asn Ile Met Leu Leu Leu Gly Gly Phe Asn Thr Asn Asn Met Asn Met
260 265 270

Ser Arg Ala Ser Val Tyr Ala Ala His Thr Leu Ala Gly Thr Ser Val
275 280 285

Gln Asn Ile Leu His Trp Ser Gln Ala Val Asn Ser Gly Glu Leu Arg
290 295 300

Ala Phe Asp Trp Gly Ser Glu Thr Lys Asn Leu Glu Lys Cys Asn Gln
305 310 315 320

Pro Thr Pro Val Arg Tyr Arg Val Arg Asp Met Thr Val Pro Thr Ala
325 330 335

Met Trp Thr Gly Gly Gln Asp Trp Leu Ser Asn Pro Glu Asp Val Lys
340 345 350

Met Leu Leu Ser Glu Val Thr Asn Leu Ile Tyr His Lys Asn Ile Pro
355 360 365

Glu Trp Ala His Val Asp Phe Ile Trp Gly Leu Asp Ala Pro His Arg
370 375 380

Met Tyr Asn Glu Ile Ile His Leu Met Gln Gln Glu Glu Thr Asn Leu
385 390 395 400

Ser Gln Gly Arg Cys Glu Ala Val Leu
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<222> (82)..(921)

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Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp
1 5 10

atg	ctg	gat	gat	gat	ggg	gac	acc	acc	atg	agc	ctg	cat	tct	caa	gcc	159
Met	Leu	Asp	Asp	Asp	Gly	Asp	Thr	Thr	Met	Ser	Leu	His	Ser	Gln	Ala	
				15					20					25		
tct	gcc	aca	act	cgg	cat	cca	gag	ccc	cgg	cgc	aca	gag	cac	agg	gct	207
Ser	Ala	Thr	Thr	Arg	His	Pro	Glu	Pro	Arg	Arg	Thr	Glu	His	Arg	Ala	
			30					35					40			
ccc	tct	tca	acg	tgg	cga	cca	gtg	gcc	ctg	acc	ctg	ctg	act	ttg	tgc	255
Pro	Ser	Ser	Thr	Trp	Arg	Pro	Val	Ala	Leu	Thr	Leu	Leu	Thr	Leu	Cys	
		45					50					55				
ttg	gtg	ctg	ctg	ata	ggg	ctg	gca	gcc	ctg	ggg	ctt	ttg	ttt	ttt	cag	303
Leu	Val	Leu	Leu	Ile	Gly	Leu	Ala	Ala	Leu	Gly	Leu	Leu	Phe	Phe	Gln	
	60					65					70					
tac	tac	cag	ctc	tcc	aat	act	ggt	caa	gac	acc	att	tct	caa	atg	gaa	351
Tyr	Tyr	Gln	Leu	Ser	Asn	Thr	Gly	Gln	Asp	Thr	Ile	Ser	Gln	Met	Glu	
75					80					85					90	
gaa	aga	tta	gga	aat	acg	tcc	caa	gag	ttg	caa	tct	ctt	caa	gtc	cag	399
Glu	Arg	Leu	Gly	Asn	Thr	Ser	Gln	Glu	Leu	Gln	Ser	Leu	Gln	Val	Gln	
				95					100					105		
aat	ata	aag	ctt	gca	gga	agt	ctg	cag	cat	gtg	gct	gaa	aaa	ctc	tgt	447
Asn	Ile	Lys	Leu	Ala	Gly	Ser	Leu	Gln	His	Val	Ala	Glu	Lys	Leu	Cys	
			110					115					120			
cgt	gag	ctg	tat	aac	aaa	gct	gga	gca	cac	agg	tgc	agc	cct	tgt	aca	495
Arg	Glu	Leu	Tyr	Asn	Lys	Ala	Gly	Ala	His	Arg	Cys	Ser	Pro	Cys	Thr	
		125					130					135				
gaa	caa	tgg	aaa	tgg	cat	gga	gac	aat	tgc	tac	cag	ttc	tat	aaa	gac	543
Glu	Gln	Trp	Lys	Trp	His	Gly	Asp	Asn	Cys	Tyr	Gln	Phe	Tyr	Lys	Asp	
	140					145					150					
agc	aaa	agt	tgg	gag	gac	tgt	aaa	tat	ttc	tgc	ctt	agt	gaa	aac	tct	591
Ser	Lys	Ser	Trp	Glu	Asp	Cys	Lys	Tyr	Phe	Cys	Leu	Ser	Glu	Asn	Ser	
155					160					165					170	
acc	atg	ctg	aag	ata	aac	aaa	caa	gaa	gac	ctg	gaa	ttt	gcc	gcg	tct	639
Thr	Met	Leu	Lys	Ile	Asn	Lys	Gln	Glu	Asp	Leu	Glu	Phe	Ala	Ala	Ser	
				175					180					185		
cag	agc	tac	tct	gag	ttt	ttc	tac	tct	tat	tgg	aca	ggg	ctt	ttg	cgc	687
Gln	Ser	Tyr	Ser	Glu	Phe	Phe	Tyr	Ser	Tyr	Trp	Thr	Gly	Leu	Leu	Arg	
			190					195					200			
cct	gac	agt	ggc	aag	gcc	tgg	ctg	tgg	atg	gat	gga	acc	cct	ttc	act	735
Pro	Asp	Ser	Gly	Lys	Ala	Trp	Leu	Trp	Met	Asp	Gly	Thr	Pro	Phe	Thr	
		205					210					215				
tct	gaa	ctg	ttc	cat	att	ata	ata	gat	gtc	acc	agc	cca	aga	agc	aga	783
Ser	Glu	Leu	Phe	His	Ile	Ile	Ile	Asp	Val	Thr	Ser	Pro	Arg	Ser	Arg	
	220					225					230					
gac	tgt	gtg	gcc	atc	ctt	aat	ggg	atg	atc	ttc	tca	aag	gac	tgc	aaa	831
Asp	Cys	Val	Ala	Ile	Leu	Asn	Gly	Met	Ile	Phe	Ser	Lys	Asp	Cys	Lys	
235					240					245					250	
gaa	ttg	aag	cgt	tgt	gtc	tgt	gag	aga	agg	gca	gga	atg	gtg	aag	cca	879
Glu	Leu	Lys	Arg	Cys	Val	Cys	Glu	Arg	Arg	Ala	Gly	Met	Val	Lys	Pro	
				255					260					265		

gag agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac 921
Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp
270 275 280

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gcagtcactt	cccagattgt	accagcaaata	acacaaggaa	ttctttttgt	ttgtttcagt	1401
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ccaacaggg	atgtcacttg	atatgagaat	ctcaaatactc	aatgccttat	aagcattcct	1521
tctgtgtcc	attaagactc	tgataattgt	ctccctcca	taggaatttc	tcccaggaaa	1581
gaaatatatc	cccatctccg	tttcatatca	gaactaccgt	ccccgatatt	cccttcagag	1641
agattaaaga	ccagaaaaaa	gtgagcctct	tcatctgcac	ctgtaatagt	ttcagttcct	1701
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tgtaaatact	gtgaagtgtg	tgtgatttta	caatggactt	atggttggtg	ggaaaattca	1821
gcatggaaat	gcttttcaaa	atatgatagc	ggtcattatt	ttgattgtgc	cttactgaaa	1881
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gaggtgagct	tatggcatca	acacatgggt	gatgaggaag	ctgagttgca	ttagtgcaca	2061
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ttgtgaggca	cttctttctt	gagatgactc	catgcacaaa	tataacaggg	atcattggga	2181
atgacaccat	cacagccacc	aagnttattg	ggttactgat	aat		2224

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<210> 23
<211> 280
<212> PRT
<213> Homo sapiens
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20 25 30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
115 120 125

Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His
130 135 140

Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp
145 150 155 160

Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn
165 170 175

Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe
180 185 190

Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala
195 200 205

Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile
210 215 220

Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
225 230 235 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val
245 250 255

Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro
260 265 270

Pro Glu Thr Leu Gly Glu Gly Asp
275 280

<210> 24
<211> 996
<212> DNA
<213> Homo sapiens

<220>
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<222> (38)..(979)

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Ser Thr Met Asp Met Leu Asp Asp Gly Asp Thr Thr Met Ser Leu
10 15 20

cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc aca 151
His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg Thr
25 30 35

gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc ctg 199
Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr Leu
40 45 50

ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg ctt 247
Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu
55 60 65 70

ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc att 295
Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile
75 80 85

tct caa atg gaa gaa aga tta gga aat acg tcc caa gag ttg caa tct 343
Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser
90 95 100

ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag cat gtg gct 391
Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala
105 110 115

gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga ggc tat aca aga 439
Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly Tyr Thr Arg
120 125 130

aac atg gtg cca gca tct gct tct tct gag agc ctc agg cag ctt cca 487
Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg Gln Leu Pro
135 140 145 150

cac atg ggg gaa agt gca gca gca cac agg tgc agc cct tgt aca gaa 535
His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro Cys Thr Glu
155 160 165

caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac agc 583
Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser
170 175 180

aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct acc 631
Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr
185 190 195

atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct cag	679
Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln	
200 205 210	
agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt ttg cgc cct	727
Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro	
215 220 225 230	
gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct ttc act tct	775
Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser	
235 240 245	
gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga gac	823
Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp	
250 255 260	
tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac tgc aaa gaa	871
Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu	
265 270 275	
ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg aag cca gag	919
Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu	
280 285 290	
agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac atg cat cat	967
Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp Met His His	
295 300 305 310	
cat cat cat cat tagcctaggt tctagac	996
His His His His	

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 <212> PRT
 <213> Homo sapiens

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Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
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Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
 50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
 65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
115 120 125

Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu
130 135 140

Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg
145 150 155 160

Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr
165 170 175

Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
180 185 190

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu
195 200 205

Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp
210 215 220

Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp
225 230 235 240

Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr
245 250 255

Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe
260 265 270

Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala
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Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly
290 295 300

Glu Gly Asp Met His His His His His His
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 Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp
 1 5 10
 atg ctg gat gat gat ggg gac acc acc atg agc ctg cat tct caa gcc 159
 Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala
 15 20 25
 tct gcc aca act cgg cat cca gag ccc cgg cgc aca gtt ttt cag tac 207
 Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr
 30 35 40
 tac cag ctc tcc aat act ggt caa gac acc att tct caa atg gaa gaa 255
 Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu
 45 50 55
 aga tta gga aat acg tcc caa gag ttg caa tct ctt caa gtc cag aat 303
 Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn
 60 65 70
 ata aag ctt gca gga agt ctg cag cat gtg gct gaa aaa ctc tgt cgt 351
 Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg
 75 80 85 90
 gag ctg tat aac aaa gct gga gca cac agg tgc agc cct tgt aca gaa 399
 Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu
 95 100 105
 caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac agc 447
 Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser
 110 115 120
 aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct acc 495
 Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr
 125 130 135
 atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct cag 543
 Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln
 140 145 150
 agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt ttg cgc cct 591
 Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro
 155 160 165 170
 gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct ttc act tct 639
 Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser
 175 180 185
 gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga gac 687
 Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp
 190 195 200

tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac tgc aaa gaa	735
Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu	
205 210 215	
ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg aag cca gag	783
Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu	
220 225 230	
agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac tgattcgccc	832
Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp	
235 240 245	
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ttgggaaatg gaacataatc aggaaagact atctctctga ctagtacaaa atgggttctc	952
gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgcacg tatttaacag	1012
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attaagactc tgataattgt ctcccctcca taggaatttc tcccaggaaa gaaatatatc	1492
cccatctccg tttcatatca gaactaccgt ccccgatatt cccttcagag agattaaaga	1552
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aatttacaag agtactgatt acatgattat ctggagaaaa taagatgtct ttgaaataca	1852
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<210> 27
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<400> 27

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly
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Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
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Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser Asn Thr
35 40 45

Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser
50 55 60

Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser
65 70 75 80

Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala
85 90 95

Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly
100 105 110

Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys
115 120 125

Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys
130 135 140

Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe
145 150 155 160

Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp
165 170 175

Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile
180 185 190

Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn
195 200 205

Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys
210 215 220

Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro
225 230 235 240

Glu Thr Leu Gly Glu Gly Asp
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aagtcctagg actgatctcc aggaccagca ctcttctccc agcccttagg gtctctgctcg 180
gccaaaggcct tccctgcc atg cga cct gtc agt gtc tgg cag tgg agc ccc 231
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro
1 5 10
tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tcg tgc ttg ggg tct ccg 279
Trp Gly Leu Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro
15 20 25
tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt cgg 327
Ser Pro Ser Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg
30 35 40
ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg gag 375
Phe Arg Leu Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu
45 50 55
ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc acg 423
Ile Gln Arg Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr
60 65 70 75
ctg cag gct gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag gcc 471
Leu Gln Ala Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala
80 85 90
aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc atc 519
Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile
95 100 105
tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act gaa 567
Trp Leu Asp Asn Leu Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu
110 115 120
tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag gat 615
Cys Ala Ser Arg Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp
125 130 135
gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tcg gac tcc 663
Ala Gly Val Ile Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser
140 145 150 155
aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga att 711
Asn Val Ile Glu Val Glu His His Leu Gln Val Glu Glu Val Arg Ile
160 165 170

cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag ggg Arg Pro Ala Val Gly Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly 175 180 185	759
ctg gtg gaa gtc agg ctt cct gac ggc tgg tgc caa gtg tgc gac aaa Leu Val Glu Val Arg Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys 190 195 200	807
ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc ttc Gly Trp Ser Ala His Asn Ser His Val Val Cys Gly Met Leu Gly Phe 205 210 215	855
ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc caa Pro Ser Glu Lys Arg Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln 220 225 230 235	903
cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc acg Arg Gln Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr 240 245 250	951
gag gcc cac ctc tcc ctc tgt tcc ctg gag ttc tat cgt gcc aat gac Glu Ala His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp 255 260 265	999
acc gcc agg tgc cct ggg ggg ggc cct gca gtg gtg agc tgt gtg cca Thr Ala Arg Cys Pro Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro 270 275 280	1047
ggc cct gtc tac gcg gca tcc agt ggc cag aag aag caa caa cag tcg Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser 285 290 295	1095
aag cct cag ggg gag gtc cgt gtc cgt cta aag ggc ggc gcc cac cct Lys Pro Gln Gly Glu Val Arg Val Arg Leu Lys Gly Gly Ala His Pro 300 305 310 315	1143
gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca gtc Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val 320 325 330	1191
tgt tac cgc aag tgg gac ctg cat gca gcc agc gtg gtg tgt cgg gag Cys Tyr Arg Lys Trp Asp Leu His Ala Ala Ser Val Val Cys Arg Glu 335 340 345	1239
ctg ggc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg ggg Leu Gly Phe Gly Ser Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly 350 355 360	1287
cag ggc atg ggt gct atc cac ctg agt gaa gtt cgc tgc tct gga cag Gln Gly Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln 365 370 375	1335
gag ctc tcc ctc tgg aag tgc ccc cac aag aac atc aca gct gag gat Glu Leu Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp 380 385 390 395	1383
tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac act Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr 400 405 410	1431
ggg gca gag acc agg atc cga ctc agt ggg ggc cgc agc caa cat gag Gly Ala Glu Thr Arg Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu 415 420 425	1479

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ctc atc tgt ggg gat gac tgg ggg acc ctg gag gcc atg gtg gcc tgt Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys 445 450 455	1575
agg caa ctg ggt ctg ggc tac gcc aac cac ggc ctg cag gag acc tgg Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp 460 465 470 475	1623
tac tgg gac tct ggg aat ata aca gag gtg gtg atg agt gga gtg cgc Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser Gly Val Arg 480 485 490	1671
tgc aca ggg act gag ctg tcc ctg gat cag tgt gcc cat cat ggc acc Cys Thr Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His His Gly Thr 495 500 505	1719
cac atc acc tgc aag agg aca ggg acc cgc ttc act gct gga gtc atc His Ile Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile 510 515 520	1767
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gag acc gcc tac atc gaa gac cgg ccc ctg cat atg ttg tac tgt gct Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala 540 545 550 555	1863
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gat atc ctc acc cca aat ggc acc aag gtg gct gag ggc cac aaa gct Asp Ile Leu Thr Pro Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala 620 625 630 635	2103
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gaa gta gca gag agt gac ttt acc aac aat gca atg aaa tgt aac tgc Glu Val Ala Glu Ser Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys 700 705 710 715	2343
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gcc ttc agt gaa gag gcc aac agg agg ttt gaa cgc tac cct ggc cag Ala Phe Ser Glu Glu Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln 735 740 745	2439
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Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
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Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
65 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
100 105 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
115 120 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
130 135 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
145 150 155 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
165 170 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
180 185 190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
195 200 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
210 215 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser
225 230 235 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser
245 250 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
260 265 270

Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala
275 280 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu
290 295 300

Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val
305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Tyr Arg Lys Trp
325 330 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser
340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala
355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp
370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln
385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
405 410 415

Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val
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Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly
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His Tyr His Ser Met Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro
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Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu	
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Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp	
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Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp Trp Leu	
315 320 325 330	
act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc ttt gtt	1899
Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile Phe Val	
335 340 345	
tgt aat tcc aac ggt tct gta tgt gtc acc ctg att gat ctg gag ctt	1947
Cys Asn Ser Asn Gly Ser Val Cys Val Thr Leu Ile Asp Leu Glu Leu	
350 355 360	
cac aat cct aaa gca ata gca gta gat cca ata gca gga aaa ctt ttc	1995
His Asn Pro Lys Ala Ile Ala Val Asp Pro Ile Ala Gly Lys Leu Phe	
365 370 375	
ttt act gac tac ggg aat gtc gcc aaa gtg gag aga tgt gac atg gat	2043
Phe Thr Asp Tyr Gly Asn Val Ala Lys Val Glu Arg Cys Asp Met Asp	
380 385 390	
ggg atg aac cga aca agg ata att gat tca aag aca gag cag cca gct	2091
Gly Met Asn Arg Thr Arg Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala	
395 400 405 410	
gca ctg gca cta gac cta gtc aac aaa ttg gtt tac tgg gta gat ctt	2139
Ala Leu Ala Leu Asp Leu Val Asn Lys Leu Val Tyr Trp Val Asp Leu	
415 420 425	
tac ttg gac tat gtg gga gta gtg gac tat caa gga aaa aat aga cac	2187
Tyr Leu Asp Tyr Val Gly Val Val Asp Tyr Gln Gly Lys Asn Arg His	
430 435 440	
act gtc att caa ggc aga caa gtc aga cat ctt tat ggt ata act gtg	2235
Thr Val Ile Gln Gly Arg Gln Val Arg His Leu Tyr Gly Ile Thr Val	
445 450 455	
ttt gaa gat tat ttg tat gca acc aat tct gat aac tac aat atc gta	2283
Phe Glu Asp Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val	
460 465 470	
agg ata aac cga ttt aat ggg act gat att cac tca tta att aaa att	2331
Arg Ile Asn Arg Phe Asn Gly Thr Asp Ile His Ser Leu Ile Lys Ile	
475 480 485 490	
gag aat gct tgg gga atc cga att tat caa aaa aga act caa cca aca	2379
Glu Asn Ala Trp Gly Ile Arg Ile Tyr Gln Lys Arg Thr Gln Pro Thr	
495 500 505	
gtc aga agc cat gca tgt gaa gtc gat cca tat gga atg cca ggg ggc	2427
Val Arg Ser His Ala Cys Glu Val Asp Pro Tyr Gly Met Pro Gly Gly	
510 515 520	
tgt tca cac atc tgt cta ctc agc agc agt tac aaa act cgg act tgt	2475
Cys Ser His Ile Cys Leu Leu Ser Ser Ser Tyr Lys Thr Arg Thr Cys	
525 530 535	

cgc tgc agg act ggc ttc aac ttg gga agt gat ggc agg tca tgc aaa Arg Cys Arg Thr Gly Phe Asn Leu Gly Ser Asp Gly Arg Ser Cys Lys 540 545 550	2523
aga cca aag aat gag ttg ttc ctc ttt tat ggg aaa gga cgc cca gga Arg Pro Lys Asn Glu Leu Phe Leu Phe Tyr Gly Lys Gly Arg Pro Gly 555 560 565 570	2571
att gtt aga gga atg gac ttg aat acc aag ata gct gat gaa tac atg Ile Val Arg Gly Met Asp Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met 575 580 585	2619
atc ccc ata gaa aat ctg gta aac cct cgt gct tta gac ttt cac gca Ile Pro Ile Glu Asn Leu Val Asn Pro Arg Ala Leu Asp Phe His Ala 590 595 600	2667
gaa acc aat tac atc tac ttt gct gac acc acc agt ttc cta att ggc Glu Thr Asn Tyr Ile Tyr Phe Ala Asp Thr Thr Ser Phe Leu Ile Gly 605 610 615	2715
cgg cag aag ata gat ggc aca gag aga gaa acc atc ctg aaa gat gat Arg Gln Lys Ile Asp Gly Thr 625 Glu Arg Glu Thr Ile Leu Lys Asp Asp 620 630	2763
ctg gat aat gta gag ggc att gct gtg gac tgg att gga aat aat ctt Leu Asp Asn Val Glu Gly Ile Ala Val Asp Trp Ile Gly Asn Asn Leu 635 640 645 650	2811
tac tgg acc aat gat ggc cat agg aaa acc att aat gtg gct agg ctg Tyr Trp Thr Asn Asp Gly His Arg Lys Thr Ile Asn Val Ala Arg Leu 655 660 665	2859
gaa aaa gct tct cag agt cgg aag act ctt tta gag ggt gaa atg tct Glu Lys Ala Ser Gln Ser Arg Lys Thr Leu Leu Glu Gly Glu Met Ser 670 675 680	2907
cat ccc aga gga att gtg gtg gat cca att aat ggt tgg atg tat tgg His Pro Arg Gly Ile Val Val Asp Pro Ile Asn Gly Trp Met Tyr Trp 685 690 695	2955
aca gac tgg gag gaa gat gaa ata gat gac agc gtg gga agg att gag Thr Asp Trp Glu Glu Asp Glu Ile Asp Asp Ser Val Gly Arg Ile Glu 700 705 710	3003
aag gcc tgg atg gat gga ttc aat cgg cag att ttt gtg act tca aag Lys Ala Trp Met Asp Gly Phe Asn Arg Gln Ile Phe Val Thr Ser Lys 715 720 725 730	3051
atg ctg tgg cca aac ggt tta act ctg gac ttt cac acc aac aca tta Met Leu Trp Pro Asn Gly Leu Thr Leu Asp Phe His Thr Asn Thr Leu 735 740 745	3099
tac tgg tgt gat gcc tat tac gat cat att gaa aaa gta ttt ttg aat Tyr Trp Cys Asp Ala Tyr Tyr Asp His Ile Glu Lys Val Phe Leu Asn 750 755 760	3147
ggg act cac agg aag att gtt tac agt ggg aga gag ttg aac cac cct Gly Thr His Arg Lys Ile Val Tyr Ser Gly Arg Glu Leu Asn His Pro 765 770 775	3195
ttc gga ctg tcg cat cat gga aat tat gtg ttc tgg act gat tat atg Phe Gly Leu Ser His His Gly Asn Tyr Val Phe Trp Thr Asp Tyr Met 780 785 790	3243

aat ggt tcc att ttt caa cta gat ttg ata aca agt gag gtg aca ttg Asn Gly Ser Ile Phe Gln Leu Asp Leu Ile Thr Ser Glu Val Thr Leu 795 800 805 810	3291
ctg agg cat gaa aga cca ccc cta ttt ggg ctt cag att tat gat cca Leu Arg His Glu Arg Pro Pro Leu Phe Gly Leu Gln Ile Tyr Asp Pro 815 820 825	3339
cga aag caa caa ggt gac aat atg tgc cga gta aat aat ggg ggc tgt Arg Lys Gln Gln Gly Asp Asn Met Cys Arg Val Asn Asn Gly Gly Cys 830 835 840	3387
agt aca ctt tgc ttg gct atc cca gga ggc cgg gtg tgt gct tgt gcc Ser Thr Leu Cys Leu Ala Ile Pro Gly Gly Arg Val Cys Ala Cys Ala 845 850 855	3435
gat aat caa ctt ttg gat gaa aat ggg aca act tgc aca ttt aat cct Asp Asn Gln Leu Leu Asp Glu Asn Gly Thr Thr Cys Thr Phe Asn Pro 860 865 870	3483
gga gaa gca cta cct cac ata tgt aaa gct gga gag ttt cgc tgc aaa Gly Glu Ala Leu Pro His Ile Cys Lys Ala Gly Glu Phe Arg Cys Lys 875 880 885 890	3531
aac aga cac tgt atc caa gct cgg tgg aaa tgt gat ggc gac gat gac Asn Arg His Cys Ile Gln Ala Arg Trp Lys Cys Asp Gly Asp Asp Asp 895 900 905	3579
tgc cta gac gga agc gat gag gat tca gta aac tgc ttc aat cat agc Cys Leu Asp Gly Ser Asp Glu Asp Ser Val Asn Cys Phe Asn His Ser 910 915 920	3627
tgt cct gat gat cag ttt aaa tgc cag aat aat cgc tgc atc ccc aag Cys Pro Asp Asp Gln Phe Lys Cys Gln Asn Asn Arg Cys Ile Pro Lys 925 930 935	3675
aga tgg ctt tgt gat gga gct aat gac tgt ggg agc aat gaa gat gaa Arg Trp Leu Cys Asp Gly Ala Asn Asp Cys Gly Ser Asn Glu Asp Glu 940 945 950	3723
tcc aat caa act tgc aca gcc aga aca tgc cag gta gac cag ttt tct Ser Asn Gln Thr Cys Thr Ala Arg Thr Cys Gln Val Asp Gln Phe Ser 955 960 965 970	3771
tgc gga aat ggg cgt tgc att ccc aga gca tgg ctg tgt gac agg gaa Cys Gly Asn Gly Arg Cys Ile Pro Arg Ala Trp Leu Cys Asp Arg Glu 975 980 985	3819
gac gac tgt ggt gac cag aca gat gaa atg gca tct tgt gaa ttc cca Asp Asp Cys Gly Asp Gln Thr Asp Glu Met Ala Ser Cys Glu Phe Pro 990 995 1000	3867
act tgt gag cca cta acc caa ttc gta tgc aaa agt gga aga tgc Thr Cys Glu Pro Leu Thr Gln Phe Val Cys Lys Ser Gly Arg Cys 1005 1010 1015	3912
att agc agc aaa tgg cac tgc gac tct gat gac gac tgt ggg gac Ile Ser Ser Lys Trp His Cys Asp Ser Asp Asp Asp Cys Gly Asp 1020 1025 1030	3957
ggg agt gat gag gtg ggc tgt gtt cac tct tgc ttt gat aat cag Gly Ser Asp Glu Val Gly Cys Val His Ser Cys Phe Asp Asn Gln 1035 1040 1045	4002

ttc aga tgt	tcc agt ggc aga tgc	atc cca ggc cac tgg	gcc tgt	4047
Phe Arg Cys	Ser Ser Gly Arg Cys	Ile Pro Gly His Trp	Ala Cys	
1050	1055	1060		
gat ggt gac	aat gac tgt ggg gac	ttc agt gat gaa gcc	cag atc	4092
Asp Gly Asp	Asn Asp Cys Gly Asp	Phe Ser Asp Glu Ala	Gln Ile	
1065	1070	1075		
aat tgt act	aaa gaa gag att cat	tct cct gct ggt tgt	aac gga	4137
Asn Cys Thr	Lys Glu Glu Ile His	Ser Pro Ala Gly Cys	Asn Gly	
1080	1085	1090		
aat gaa ttt	cag tgc cac cct gat	ggg aat tgc gtt cct	gat ttg	4182
Asn Glu Phe	Gln Cys His Pro Asp	Gly Asn Cys Val Pro	Asp Leu	
1095	1100	1105		
tggt cgc tgt	gat gga gaa aaa gac	tgt gaa gat ggt agt	gat gaa	4227
Trp Arg Cys	Asp Gly Glu Lys Asp	Cys Glu Asp Gly Ser	Asp Glu	
1110	1115	1120		
aaa ggt tgc	aat ggt acc ata cga	ttg tgt gac cac aaa	acc aag	4272
Lys Gly Cys	Asn Gly Thr Ile Arg	Leu Cys Asp His Lys	Thr Lys	
1125	1130	1135		
ttt tcc tgt	tggt agt aca ggg aga	tgc atc aac aaa gca	tggt gtg	4317
Phe Ser Cys	Trp Ser Thr Gly Arg	Cys Ile Asn Lys Ala	Trp Val	
1140	1145	1150		
tgt gat gga	gat att gat tgc gaa	gat cag tca gat gaa	gat gac	4362
Cys Asp Gly	Asp Ile Asp Cys Glu	Asp Gln Ser Asp Glu	Asp Asp	
1155	1160	1165		
tgt gac agt	ttc ttg tgt gga cca	ccc aag cat cct tgt	gct aat	4407
Cys Asp Ser	Phe Leu Cys Gly Pro	Pro Lys His Pro Cys	Ala Asn	
1170	1175	1180		
gac acc tca	gtc tgc ctg cag cca	gag aaa ctc tgc aat	ggg aaa	4452
Asp Thr Ser	Val Cys Leu Gln Pro	Glu Lys Leu Cys Asn	Gly Lys	
1185	1190	1195		
aag gat tgt	cct gat ggc tct gat	gaa ggc tat ctc tgt	gat gag	4497
Lys Asp Cys	Pro Asp Gly Ser Asp	Glu Gly Tyr Leu Cys	Asp Glu	
1200	1205	1210		
tgt tcg ctg	aac aat gga ggc tgt	agc aac cac tgt tct	gtt gtt	4542
Cys Ser Leu	Asn Asn Gly Gly Cys	Ser Asn His Cys Ser	Val Val	
1215	1220	1225		
cct gga aga	gga att gtc tgt tcc	tgc cct gaa gga ctt	caa ctc	4587
Pro Gly Arg	Gly Ile Val Cys Ser	Cys Pro Glu Gly Leu	Gln Leu	
1230	1235	1240		
aac aaa gac	aat aaa aca tgt gaa	att gtg gat tat tgt	agc aat	4632
Asn Lys Asp	Asn Lys Thr Cys Glu	Ile Val Asp Tyr Cys	Ser Asn	
1245	1250	1255		
cat cta aag	tgc agc caa gta tgt	gag cag cac aag cac	aca gtc	4677
His Leu Lys	Cys Ser Gln Val Cys	Glu Gln His Lys His	Thr Val	
1260	1265	1270		
aag tgc tca	tgt tat gaa ggt tgg	aag ctg gat gta gac	ggg gaa	4722
Lys Cys Ser	Cys Tyr Glu Gly Trp	Lys Leu Asp Val Asp	Gly Glu	
1275	1280	1285		

agt tgt aca	agt gtt gat cct ttt	gaa gca ttc atc atc	ttt tct	4767
Ser Cys Thr	Ser Val Asp Pro Phe	Glu Ala Phe Ile Ile	Phe Ser	
1290	1295	1300		
att cgt cat	gag atc aga agg att	gat ctt cac aaa aga	gac tat	4812
Ile Arg His	Glu Ile Arg Arg Ile	Asp Leu His Lys Arg	Asp Tyr	
1305	1310	1315		
agt cta ctt	gtt cct gga ttg aga	aac aca ata gca ctt	gat ttt	4857
Ser Leu Leu	Val Pro Gly Leu Arg	Asn Thr Ile Ala Leu	Asp Phe	
1320	1325	1330		
cac ttc aat	caa agt tta ctt tat	tgg aca gat gtt gta	gaa gac	4902
His Phe Asn	Gln Ser Leu Leu Tyr	Trp Thr Asp Val Val	Glu Asp	
1335	1340	1345		
aga ata tac	cgg gga aag ctt tct	gaa agt gga ggt gtc	agt gcc	4947
Arg Ile Tyr	Arg Gly Lys Leu Ser	Glu Ser Gly Gly Val	Ser Ala	
1350	1355	1360		
att gaa gtg	gtt gtg gag cat ggc	ctg gct act cca gaa	ggc ctg	4992
Ile Glu Val	Val Val Glu His Gly	Leu Ala Thr Pro Glu	Gly Leu	
1365	1370	1375		
aca gtc gac	tgg ata gca gga aac	ata tac tgg ata gac	agc aat	5037
Thr Val Asp	Trp Ile Ala Gly Asn	Ile Tyr Trp Ile Asp	Ser Asn	
1380	1385	1390		
ctg gac caa	atc gaa gtg gcc aaa	cta gat ggc tcc cta	aga act	5082
Leu Asp Gln	Ile Glu Val Ala Lys	Leu Asp Gly Ser Leu	Arg Thr	
1395	1400	1405		
aca cta ata	gca gga gcc atg gaa	cac ccc agg gcc att	gct ttg	5127
Thr Leu Ile	Ala Gly Ala Met Glu	His Pro Arg Ala Ile	Ala Leu	
1410	1415	1420		
gac cca aga	tat gga att ctt ttc	tgg aca gac tgg gat	gca aat	5172
Asp Pro Arg	Tyr Gly Ile Leu Phe	Trp Thr Asp Trp Asp	Ala Asn	
1425	1430	1435		
ttt cct cgc	att gaa tct gcc tct	atg agt ggt gct ggg	aga aaa	5217
Phe Pro Arg	Ile Glu Ser Ala Ser	Met Ser Gly Ala Gly	Arg Lys	
1440	1445	1450		
acc atc tat	aaa gac atg aaa act	ggg gct tgg cct aat	gga cta	5262
Thr Ile Tyr	Lys Asp Met Lys Thr	Gly Ala Trp Pro Asn	Gly Leu	
1455	1460	1465		
act gtg gac	cac ttt gag aaa agg	ata gtg tgg aca gac	gcc agg	5307
Thr Val Asp	His Phe Glu Lys Arg	Ile Val Trp Thr Asp	Ala Arg	
1470	1475	1480		
tca gat gct	att tat tca gcc ctg	tat gat gga aca aac	atg ata	5352
Ser Asp Ala	Ile Tyr Ser Ala Leu	Tyr Asp Gly Thr Asn	Met Ile	
1485	1490	1495		
gaa atc atc	cga ggt cat gaa tac	ctt tcc cat ccc ttt	gct gtg	5397
Glu Ile Ile	Arg Gly His Glu Tyr	Leu Ser His Pro Phe	Ala Val	
1500	1505	1510		
tct cta tat	ggg agt gaa gtc tac	tgg aca gac tgg agg	acc aac	5442
Ser Leu Tyr	Gly Ser Glu Val Tyr	Trp Thr Asp Trp Arg	Thr Asn	
1515	1520	1525		

aca ttg tcc	aaa gcc aat aag tgg	aca ggg cag aat gtc	agt gtg	5487
Thr Leu Ser	Lys Ala Asn Lys Trp	Thr Gly Gln Asn Val	Ser Val	
1530	1535	1540		
att cag aaa	acc agt gca cag cca	ttt gac ctt cag ata	tac cat	5532
Ile Gln Lys	Thr Ser Ala Gln Pro	Phe Asp Leu Gln Ile	Tyr His	
1545	1550	1555		
ccc agt cgc	cag cca cag gct ccc	aat cct tgt gca gct	aat gat	5577
Pro Ser Arg	Gln Pro Gln Ala Pro	Asn Pro Cys Ala Ala	Asn Asp	
1560	1565	1570		
ggc aaa ggc	ccc tgc tct cac atg	tgt cta atc aat cac	aat agg	5622
Gly Lys Gly	Pro Cys Ser His Met	Cys Leu Ile Asn His	Asn Arg	
1575	1580	1585		
agt gct gcc	tgt gcg tgc ccc cac	ttg atg aag ctt tct	tca gac	5667
Ser Ala Ala	Cys Ala Cys Pro His	Leu Met Lys Leu Ser	Ser Asp	
1590	1595	1600		
aag aag acc	tgc tat gaa atg aaa	aaa ttt ctt ctt tat	gca aga	5712
Lys Lys Thr	Cys Tyr Glu Met Lys	Lys Phe Leu Leu Tyr	Ala Arg	
1605	1610	1615		
cgt tct gaa	atc aga gga gtg gat	att gac aat cca tac	ttt aac	5757
Arg Ser Glu	Ile Arg Gly Val Asp	Ile Asp Asn Pro Tyr	Phe Asn	
1620	1625	1630		
ttc atc acg	gca ttt aca gtc cct	gat att gat gac gtt	act gtg	5802
Phe Ile Thr	Ala Phe Thr Val Pro	Asp Ile Asp Asp Val	Thr Val	
1635	1640	1645		
ata gac ttc	gat gca tct gag gaa	cgt tta tac tgg aca	gat att	5847
Ile Asp Phe	Asp Ala Ser Glu Glu	Arg Leu Tyr Trp Thr	Asp Ile	
1650	1655	1660		
aaa aca caa	acc att aaa cga gct	ttt att aac gga act	ggg tta	5892
Lys Thr Gln	Thr Ile Lys Arg Ala	Phe Ile Asn Gly Thr	Gly Leu	
1665	1670	1675		
gaa act gtt	att tca aga gat att	cag agt atc aga ggg	cta gca	5937
Glu Thr Val	Ile Ser Arg Asp Ile	Gln Ser Ile Arg Gly	Leu Ala	
1680	1685	1690		
gtg gat tgg	gtg tca cgt aat tta	tac tgg att agc tca	gaa ttt	5982
Val Asp Trp	Val Ser Arg Asn Leu	Tyr Trp Ile Ser Ser	Glu Phe	
1695	1700	1705		
gat gaa acg	caa att aat gtg gca	agg cta gat ggc tct	ttg aaa	6027
Asp Glu Thr	Gln Ile Asn Val Ala	Arg Leu Asp Gly Ser	Leu Lys	
1710	1715	1720		
acc tca att	atc cat gga atc gat	aag cca cag tgt ctt	gca gct	6072
Thr Ser Ile	Ile His Gly Ile Asp	Lys Pro Gln Cys Leu	Ala Ala	
1725	1730	1735		
cac cca gtc	agg gga aaa ctc tac	tgg acc gat gga aac	aca att	6117
His Pro Val	Arg Gly Lys Leu Tyr	Trp Thr Asp Gly Asn	Thr Ile	
1740	1745	1750		
aac atg gca	aat atg gat ggc agt	aat agc aag att ctg	ttt cag	6162
Asn Met Ala	Asn Met Asp Gly Ser	Asn Ser Lys Ile Leu	Phe Gln	
1755	1760	1765		

aat cag aag gag cca gtt ggt cta tcg ata gac tat gtg gaa aac	6207
Asn Gln Lys Glu Pro Val Gly Leu Ser Ile Asp Tyr Val Glu Asn	
1770 1775 1780	
aag ctt tat tgg atc agt tcg ggg aat gga acc ata aat aga tgc	6252
Lys Leu Tyr Trp Ile Ser Ser Gly Asn Gly Thr Ile Asn Arg Cys	
1785 1790 1795	
aac ctg gat ggt ggt aat tta gaa gta atc gag tca atg aaa gaa	6297
Asn Leu Asp Gly Gly Asn Leu Glu Val Ile Glu Ser Met Lys Glu	
1800 1805 1810	
gaa tta aca aaa gct aca gcc cta acc atc atg gat aag aaa ctg	6342
Glu Leu Thr Lys Ala Thr Ala Leu Thr Ile Met Asp Lys Lys Leu	
1815 1820 1825	
tgg tgg gca gac caa aac tta gcc cag cta gga acc tgc agc aaa	6387
Trp Trp Ala Asp Gln Asn Leu Ala Gln Leu Gly Thr Cys Ser Lys	
1830 1835 1840	
aga gac gga aga aac ccc acc atc cta cgg aat aag act tct ggg	6432
Arg Asp Gly Arg Asn Pro Thr Ile Leu Arg Asn Lys Thr Ser Gly	
1845 1850 1855	
gta gtt cat atg aaa gtc tat gat aaa gaa gca cag caa ggc agc	6477
Val Val His Met Lys Val Tyr Asp Lys Glu Ala Gln Gln Gly Ser	
1860 1865 1870	
aat tcc tgc caa cta aac aat ggt gga tgc tct caa ctt tgt tta	6522
Asn Ser Cys Gln Leu Asn Asn Gly Gly Cys Ser Gln Leu Cys Leu	
1875 1880 1885	
cca aca tct gaa act aca agg act tgt atg tgt aca gtg gga tat	6567
Pro Thr Ser Glu Thr Thr Arg Thr Cys Met Cys Thr Val Gly Tyr	
1890 1895 1900	
tat ctc caa aag aac cgt atg tca tgt caa ggt ata gaa tca ttt	6612
Tyr Leu Gln Lys Asn Arg Met Ser Cys Gln Gly Ile Glu Ser Phe	
1905 1910 1915	
ctt atg tac tct gtt cat gaa gga atc agg gga ata cct ctt gaa	6657
Leu Met Tyr Ser Val His Glu Gly Ile Arg Gly Ile Pro Leu Glu	
1920 1925 1930	
cca agt gac aaa atg gat gct ttg atg cct ata tca gga act tca	6702
Pro Ser Asp Lys Met Asp Ala Leu Met Pro Ile Ser Gly Thr Ser	
1935 1940 1945	
ttt gcc gtg gga ata gat ttc cat gca gaa aat gat acc atc tac	6747
Phe Ala Val Gly Ile Asp Phe His Ala Glu Asn Asp Thr Ile Tyr	
1950 1955 1960	
tgg aca gac atg ggc ttc aat aaa att agc aga gct aaa aga gat	6792
Trp Thr Asp Met Gly Phe Asn Lys Ile Ser Arg Ala Lys Arg Asp	
1965 1970 1975	
cag act tgg aaa gaa gat atc att acc aat ggc ttg gga aga gtg	6837
Gln Thr Trp Lys Glu Asp Ile Ile Thr Asn Gly Leu Gly Arg Val	
1980 1985 1990	
gaa ggg ata gct gtt gac tgg att gct ggt aac ata tat tgg aca	6882
Glu Gly Ile Ala Val Asp Trp Ile Ala Gly Asn Ile Tyr Trp Thr	
1995 2000 2005	

gat cat ggt ttc aac tta att gaa gtt gca aga ctc aat ggt tct Asp His Gly Phe Asn Leu Ile Glu Val Ala Arg Leu Asn Gly Ser 2010 2015 2020	6927
ttc cgt tat gta att att tcc caa ggc ctg gat caa cca aga tct Phe Arg Tyr Val Ile Ile Ser Gln Gly Leu Asp Gln Pro Arg Ser 2025 2030 2035	6972
ata gct gtg cac cca gag aaa ggc ctc ttg ttc tgg act gaa tgg Ile Ala Val His Pro Glu Lys Gly Leu Leu Phe Trp Thr Glu Trp 2040 2045 2050	7017
gga caa atg ccc tgt att gga aag gct cgc ttg gat ggc tca gag Gly Gln Met Pro Cys Ile Gly Lys Ala Arg Leu Asp Gly Ser Glu 2055 2060 2065	7062
aag gtt gtc ctt gta agc atg gga ata gca tgg ccg aat ggc atc Lys Val Val Leu Val Ser Met Gly Ile Ala Trp Pro Asn Gly Ile 2070 2075 2080	7107
tcc atc gac tat gag gaa aat aaa ttg tac tgg tgt gat gct cgc Ser Ile Asp Tyr Glu Glu Asn Lys Leu Tyr Trp Cys Asp Ala Arg 2085 2090 2095	7152
aca gac aag ata gag aga atc gac ctt gag act gga ggg aat cgc Thr Asp Lys Ile Glu Arg Ile Asp Leu Glu Thr Gly Gly Asn Arg 2100 2105 2110	7197
gag atg gtg ctg tca gga agc aat gtg gat atg ttt tca gtt gca Glu Met Val Leu Ser Gly Ser Asn Val Asp Met Phe Ser Val Ala 2115 2120 2125	7242
gtc ttt ggg gct tac atc tac tgg tct gac aga gca cat gca aac Val Phe Gly Ala Tyr Ile Tyr Trp Ser Asp Arg Ala His Ala Asn 2130 2135 2140	7287
ggg tct gtc aga agg ggc cac aag aat gat gcc aca gaa acg ata Gly Ser Val Arg Arg Gly His Lys Asn Asp Ala Thr Glu Thr Ile 2145 2150 2155	7332
acc atg aga acc ggc ctt gga gtc aac ctg aag gag gtt aaa ata Thr Met Arg Thr Gly Leu Gly Val Asn Leu Lys Glu Val Lys Ile 2160 2165 2170	7377
ttt aac cga gta aga gag aaa ggg acc aat gtt tgt gcc agg gac Phe Asn Arg Val Arg Glu Lys Gly Thr Asn Val Cys Ala Arg Asp 2175 2180 2185	7422
aat ggt ggc tgt aag caa ctc tgt ctt tat cga gga aat tcc cgg Asn Gly Gly Cys Lys Gln Leu Cys Leu Tyr Arg Gly Asn Ser Arg 2190 2195 2200	7467
aga act tgt gct tgt gcc cat gga tat ttg gca gaa gat gga gtt Arg Thr Cys Ala Cys Ala His Gly Tyr Leu Ala Glu Asp Gly Val 2205 2210 2215	7512
act tgc ctg agg cat gaa ggc tat tta ctg tat tca gga aga aca Thr Cys Leu Arg His Glu Gly Tyr Leu Leu Tyr Ser Gly Arg Thr 2220 2225 2230	7557
ata tta aaa agt ata cat ctt tct gat gaa acc aat tta aat tcc Ile Leu Lys Ser Ile His Leu Ser Asp Glu Thr Asn Leu Asn Ser 2235 2240 2245	7602

cca ata agg	cca tat gag aat	cca cgt tat ttc aag aat	gtc ata	7647
Pro Ile Arg	Pro Tyr Glu Asn	Pro Arg Tyr Phe Lys Asn	Val Ile	
2250	2255	2260		
gcc ttg gct	ttt gac tat aat	caa aga aga aaa ggt acc	aac cga	7692
Ala Leu Ala	Phe Asp Tyr Asn	Gln Arg Arg Lys Gly Thr	Asn Arg	
2265	2270	2275		
atc ttt tac	agt gat gca cac	ttt gga aat ata cag ctt	att aaa	7737
Ile Phe Tyr	Ser Asp Ala His	Phe Gly Asn Ile Gln Leu	Ile Lys	
2280	2285	2290		
gac aac tgg	gaa gac aga caa	gta att gtt gaa aat	gtg ggt tct	7782
Asp Asn Trp	Glu Asp Arg Gln	Val Ile Val Glu Asn	Val Gly Ser	
2295	2300	2305		
gtg gaa gga	ctt gcc tat cac	aga gcc tgg gat aca	ctg tac tgg	7827
Val Glu Gly	Leu Ala Tyr His	Arg Ala Trp Asp Thr	Leu Tyr Trp	
2310	2315	2320		
aca agc tct	acc acc tca tcc	atc acc aga cac act	gtg gac cag	7872
Thr Ser Ser	Thr Thr Ser Ser	Ile Thr Arg His Thr	Val Asp Gln	
2325	2330	2335		
act cgg cct	gga gca ttt gac	agg gaa gct gtc atc	acc atg tca	7917
Thr Arg Pro	Gly Ala Phe Asp	Arg Glu Ala Val Ile	Thr Met Ser	
2340	2345	2350		
gaa gat gac	cat cca cat gtg	cta gcc ttg gat gaa	tgt caa aat	7962
Glu Asp Asp	His Pro His Val	Leu Ala Leu Asp Glu	Cys Gln Asn	
2355	2360	2365		
tta atg ttt	tgg acc aac tgg	aat gaa caa cat cca	agt atc atg	8007
Leu Met Phe	Trp Thr Asn Trp	Asn Glu Gln His Pro	Ser Ile Met	
2370	2375	2380		
aga tct act	ctg act ggg aaa	aat gct caa gtg gtg	gtc agt aca	8052
Arg Ser Thr	Leu Thr Gly Lys	Asn Ala Gln Val Val	Val Ser Thr	
2385	2390	2395		
gac ata ctc	act cca aat gga	ctt act atc gac tac	cgt gca gag	8097
Asp Ile Leu	Thr Pro Asn Gly	Leu Thr Ile Asp Tyr	Arg Ala Glu	
2400	2405	2410		
aag ctg tat	ttc tca gat ggc	agt cta gga aaa att	gaa agg tgt	8142
Lys Leu Tyr	Phe Ser Asp Gly	Ser Leu Gly Lys Ile	Glu Arg Cys	
2415	2420	2425		
gaa tac gat	gga tcc cag aga	cat gtg ata gtt aaa	tct ggg cca	8187
Glu Tyr Asp	Gly Ser Gln Arg	His Val Ile Val Lys	Ser Gly Pro	
2430	2435	2440		
ggg act ttc	ctc agt ttg gct	gtt tat gac aat tat	ata ttc tgg	8232
Gly Thr Phe	Leu Ser Leu Ala	Val Tyr Asp Asn Tyr	Ile Phe Trp	
2445	2450	2455		
tcg gac tgg	gga aga aga gct	ata ctg cgg tcc aac	aag tac aca	8277
Ser Asp Trp	Gly Arg Arg Ala	Ile Leu Arg Ser Asn	Lys Tyr Thr	
2460	2465	2470		
gga gga gat	aca aaa att ctt	cgt tcc gat att cca	cat cag cca	8322
Gly Gly Asp	Thr Lys Ile Leu	Arg Ser Asp Ile Pro	His Gln Pro	
2475	2480	2485		

atg gga atc	ata gct gtt gcc	aat gac acc	aat agc tgt	gaa ctt	8367
Met Gly Ile	Ile Ala Val Ala	Asn Asp Thr Asn	Ser Cys Glu Leu		
2490	2495	2500			
tct cca tgt	gca tta ttg aat	gga ggc tgc	cat gac ttg	tgc ctt	8412
Ser Pro Cys	Ala Leu Leu Asn	Gly Gly Cys His	Asp Leu Cys Leu		
2505	2510	2515			
tta act ccc	aat ggg aga gtg	aat tgt tcc tgc	aga ggg gac	cga	8457
Leu Thr Pro	Asn Gly Arg Val	Asn Cys Ser Cys	Arg Gly Asp Arg		
2520	2525	2530			
ata ttg cta	gag gac aac aga	tgt gtg act	aaa aat tcc	tcc tgc	8502
Ile Leu Leu	Glu Asp Asn Arg	Cys Val Thr Lys	Asn Ser Ser Cys		
2535	2540	2545			
aac gct tat	tcg gag ttt gaa	tgt gga aat	ggt gag tgc	att gac	8547
Asn Ala Tyr	Ser Glu Phe Glu	Cys Gly Asn Gly	Glu Cys Ile Asp		
2550	2555	2560			
tac cag ctc	acc tgt gat ggc	att cct cac	tgt aaa gat	aaa tca	8592
Tyr Gln Leu	Thr Cys Asp Gly	Ile Pro His Cys	Lys Asp Lys Ser		
2565	2570	2575			
gat gaa aaa	ctg ctc tac tgt	gaa aac aga	agc tgt cga	aga ggc	8637
Asp Glu Lys	Leu Leu Tyr Cys	Glu Asn Arg Ser	Cys Arg Arg Gly		
2580	2585	2590			
ttc aag cca	tgc tat aat cgc	cgc tgc att	cct cat ggc	aag tta	8682
Phe Lys Pro	Cys Tyr Asn Arg	Arg Cys Ile Pro	His Gly Lys Leu		
2595	2600	2605			
tgt gat gga	gaa aat gac tgc	gga gac aac	tct gat gaa	tta gat	8727
Cys Asp Gly	Glu Asn Asp Cys	Gly Asp Asn Ser	Asp Glu Leu Asp		
2610	2615	2620			
tgt aaa gtt	tca acc tgt gcc	acg gtt gag	ttc cgc tgt	gca gat	8772
Cys Lys Val	Ser Thr Cys Ala	Thr Val Glu Phe	Arg Cys Ala Asp		
2625	2630	2635			
ggg act tgt	att cca aga tca	gca cga tgc	aac cag aac	ata gat	8817
Gly Thr Cys	Ile Pro Arg Ser	Ala Arg Cys Asn	Gln Asn Ile Asp		
2640	2645	2650			
tgt gca gat	gct tca gat gaa	aag aac tgc	aat aac aca	gac tgc	8862
Cys Ala Asp	Ala Ser Asp Glu	Lys Asn Cys Asn	Asn Thr Asp Cys		
2655	2660	2665			
aca cat ttc	tat aag ctt gga	gtg aaa acc	aca ggg ttc	ata aga	8907
Thr His Phe	Tyr Lys Leu Gly	Val Lys Thr Thr	Gly Phe Ile Arg		
2670	2675	2680			
tgt aat tct	acc tca ctg tgt	gtt ctg cca	acc tgg ata	tgc gac	8952
Cys Asn Ser	Thr Ser Leu Cys	Val Leu Pro Thr	Trp Ile Cys Asp		
2685	2690	2695			
ggg tct aat	gac tgt gga gac	tat tca gat	gaa tta aag	tgc cca	8997
Gly Ser Asn	Asp Cys Gly Asp	Tyr Ser Asp Glu	Leu Lys Cys Pro		
2700	2705	2710			
gtt cag aac	aaa cac aaa tgt	gaa gaa aat	tat ttt agt	tgt cct	9042
Val Gln Asn	Lys His Lys Cys	Glu Glu Asn Tyr	Phe Ser Cys Pro		
2715	2720	2725			

agt gga aga tgc att ttg aat acc tgg ata tgc gat ggt cag aaa	9087
Ser Gly Arg Cys Ile Leu Asn Thr Trp Ile Cys Asp Gly Gln Lys	
2730 2735 2740	
gat tgt gag gat gga cgt gat gaa ttc cac tgt gat tct tct tgc	9132
Asp Cys Glu Asp Gly Arg Asp Glu Phe His Cys Asp Ser Ser Cys	
2745 2750 2755	
tct tgg aac caa ttt gct tgt tcc gca caa aaa tgt att tct aag	9177
Ser Trp Asn Gln Phe Ala Cys Ser Ala Gln Lys Cys Ile Ser Lys	
2760 2765 2770	
cat tgg att tgt gat gga gaa gat gac tgt ggg gat ggg tta gat	9222
His Trp Ile Cys Asp Gly Glu Asp Asp Cys Gly Asp Gly Leu Asp	
2775 2780 2785	
gaa agt gac agc att tgt ggt gcc ata acc tgt gct gct gac atg	9267
Glu Ser Asp Ser Ile Cys Gly Ala Ile Thr Cys Ala Ala Asp Met	
2790 2795 2800	
ttc agc tgc cag ggc tct cgt gcc tgc gtg ccc cga cat tgg ctt	9312
Phe Ser Cys Gln Gly Ser Arg Ala Cys Val Pro Arg His Trp Leu	
2805 2810 2815	
tgt gat ggt gaa agg gac tgt cca gat gga agc gat gag ctt tcc	9357
Cys Asp Gly Glu Arg Asp Cys Pro Asp Gly Ser Asp Glu Leu Ser	
2820 2825 2830	
aca gca ggc tgc gct ccc aat aat aca tgt gat gaa aat gct ttc	9402
Thr Ala Gly Cys Ala Pro Asn Asn Thr Cys Asp Glu Asn Ala Phe	
2835 2840 2845	
atg tgc cat aat aaa gta tgc att ccc aag caa ttt gtt tgt gac	9447
Met Cys His Asn Lys Val Cys Ile Pro Lys Gln Phe Val Cys Asp	
2850 2855 2860	
cat gat gac gac tgt gga gat ggc tct gat gag tca ccg cag tgt	9492
His Asp Asp Asp Cys Gly Asp Gly Ser Asp Glu Ser Pro Gln Cys	
2865 2870 2875	
gga tac cga cag tgt ggt aca gaa gaa ttt agt tgt gct gat ggg	9537
Gly Tyr Arg Gln Cys Gly Thr Glu Glu Phe Ser Cys Ala Asp Gly	
2880 2885 2890	
cgg tgt ctt cta aat act caa tgg cag tgt gat gga gac ttt gac	9582
Arg Cys Leu Leu Asn Thr Gln Trp Gln Cys Asp Gly Asp Phe Asp	
2895 2900 2905	
tgt cct gac cat tct gat gaa gca cct tta aac cca aag tgt aaa	9627
Cys Pro Asp His Ser Asp Glu Ala Pro Leu Asn Pro Lys Cys Lys	
2910 2915 2920	
agt gca gaa cag tca tgc aac agt tca ttt ttt atg tgc aaa aat	9672
Ser Ala Glu Gln Ser Cys Asn Ser Ser Phe Phe Met Cys Lys Asn	
2925 2930 2935	
ggc agg tgc att ccc agt gga ggt ctt tgt gac aat aag gat gac	9717
Gly Arg Cys Ile Pro Ser Gly Gly Leu Cys Asp Asn Lys Asp Asp	
2940 2945 2950	
tgt ggc gat ggt tca gat gag aga aac tgc cat ata aat gaa tgt	9762
Cys Gly Asp Gly Ser Asp Glu Arg Asn Cys His Ile Asn Glu Cys	
2955 2960 2965	

ttg agt aag	aaa gtc agt gga tgt	tct caa gat tgt caa gac ctt	9807
Leu Ser Lys	Lys Val Ser Gly Cys	Ser Gln Asp Cys Gln Asp Leu	
2970	2975	2980	
ccg gtc agt	tat aag tgc aaa tgc	tgg cct gga ttc caa ctg aag	9852
Pro Val Ser	Tyr Lys Cys Lys Cys	Trp Pro Gly Phe Gln Leu Lys	
2985	2990	2995	
gat gac ggc	aaa aca tgt gta gac	att gat gaa tgc tct tca ggc	9897
Asp Asp Gly	Lys Thr Cys Val Asp	Ile Asp Glu Cys Ser Ser Gly	
3000	3005	3010	
ttt ccc tgt	agc cag caa tgc atc	aat aca tac ggg act tac aag	9942
Phe Pro Cys	Ser Gln Gln Cys Ile	Asn Thr Tyr Gly Thr Tyr Lys	
3015	3020	3025	
tgc ctc tgt	aca gat ggg tat gaa	ata caa cct gat aac cca aat	9987
Cys Leu Cys	Thr Asp Gly Tyr Glu	Ile Gln Pro Asp Asn Pro Asn	
3030	3035	3040	
ggc tgc aaa	tcg ctc tca gat gaa	gaa cct ttt tta att ctt gct	10032
Gly Cys Lys	Ser Leu Ser Asp Glu	Glu Pro Phe Leu Ile Leu Ala	
3045	3050	3055	
gat cat cat	gag ata agg aaa att	agc act gat ggc tcc aac tac	10077
Asp His His	Glu Ile Arg Lys Ile	Ser Thr Asp Gly Ser Asn Tyr	
3060	3065	3070	
aca ctt tta	aaa cag gga tta aac	aat gtt att gct ata gac ttt	10122
Thr Leu Leu	Lys Gln Gly Leu Asn	Asn Val Ile Ala Ile Asp Phe	
3075	3080	3085	
gat tac aga	gaa gaa ttc atc tat	tgg atc gat tct agc cga ccc	10167
Asp Tyr Arg	Glu Glu Phe Ile Tyr	Trp Ile Asp Ser Ser Arg Pro	
3090	3095	3100	
aat ggc agt	cgc ata aat aga atg	tgt tta aat gga agt gac att	10212
Asn Gly Ser	Arg Ile Asn Arg Met	Cys Leu Asn Gly Ser Asp Ile	
3105	3110	3115	
aag gta gtt	cat aac aca gcg gtc	ccc aat gca ctt gct gtc gat	10257
Lys Val Val	His Asn Thr Ala Val	Pro Asn Ala Leu Ala Val Asp	
3120	3125	3130	
tgg att gga	aaa aac ctc tat tgg	tct gac aca gaa aaa aga atc	10302
Trp Ile Gly	Lys Asn Leu Tyr Trp	Ser Asp Thr Glu Lys Arg Ile	
3135	3140	3145	
att gaa gta	tcc aaa ctc aat ggc	ttg tac cct act ata ctc gtt	10347
Ile Glu Val	Ser Lys Leu Asn Gly	Leu Tyr Pro Thr Ile Leu Val	
3150	3155	3160	
agc aaa agg	ctg aag ttt ccc aga	gac ttg tct tta gat cct caa	10392
Ser Lys Arg	Leu Lys Phe Pro Arg	Asp Leu Ser Leu Asp Pro Gln	
3165	3170	3175	
gct gga tat	ttg tat tgg att gac	tgc tgc gag tat cct cat att	10437
Ala Gly Tyr	Leu Tyr Trp Ile Asp	Cys Cys Glu Tyr Pro His Ile	
3180	3185	3190	
ggc cgt gtt	gga atg gat gga acc	aat cag agt gtt gtc ata gaa	10482
Gly Arg Val	Gly Met Asp Gly Thr	Asn Gln Ser Val Val Ile Glu	
3195	3200	3205	

acc aag att tct aga cct atg gca cta aca ata gat tat gtt aat	10527
Thr Lys Ile Ser Arg Pro Met Ala Leu Thr Ile Asp Tyr Val Asn	
3210 3215 3220	
cgt aga ctc tac tgg gcc gat gaa aat cac att gaa ttt agc aac	10572
Arg Arg Leu Tyr Trp Ala Asp Glu Asn His Ile Glu Phe Ser Asn	
3225 3230 3235	
atg gat gga tct cat aga cac aaa gtc cct aat caa gat att cca	10617
Met Asp Gly Ser His Arg His Lys Val Pro Asn Gln Asp Ile Pro	
3240 3245 3250	
ggg gtg att gca cta aca ttg ttt gaa gac tac atc tac tgg act	10662
Gly Val Ile Ala Leu Thr Leu Phe Glu Asp Tyr Ile Tyr Trp Thr	
3255 3260 3265	
gat ggg aaa acc aag tca ctc agc cgt gcc cat aaa aca tcg gga	10707
Asp Gly Lys Thr Lys Ser Leu Ser Arg Ala His Lys Thr Ser Gly	
3270 3275 3280	
gca gac aga ctc tca ctg att tac tca tgg cat gcc atc aca gat	10752
Ala Asp Arg Leu Ser Leu Ile Tyr Ser Trp His Ala Ile Thr Asp	
3285 3290 3295	
atc cag gtg tat cat tct tat aga caa cct gat gtc tcc aaa cat	10797
Ile Gln Val Tyr His Ser Tyr Arg Gln Pro Asp Val Ser Lys His	
3300 3305 3310	
ctc tgc atg ata aat aat ggt ggt tgc agt cat ttg tgc ctt tta	10842
Leu Cys Met Ile Asn Asn Gly Gly Cys Ser His Leu Cys Leu Leu	
3315 3320 3325	
gcc cct gga aaa acc cac act tgt gca tgt ccc act aac ttc tat	10887
Ala Pro Gly Lys Thr His Thr Cys Ala Cys Pro Thr Asn Phe Tyr	
3330 3335 3340	
ctg gca gct gat aat agg act tgc tta tcc aac tgc aca gcc agc	10932
Leu Ala Ala Asp Asn Arg Thr Cys Leu Ser Asn Cys Thr Ala Ser	
3345 3350 3355	
cag ttt cgt tgc aaa act gac aaa tgt att cca ttc tgg tgg aaa	10977
Gln Phe Arg Cys Lys Thr Asp Lys Cys Ile Pro Phe Trp Trp Lys	
3360 3365 3370	
tgt gac acc gtg gat gac tgt ggt gat gga tct gat gaa cct gat	11022
Cys Asp Thr Val Asp Asp Cys Gly Asp Gly Ser Asp Glu Pro Asp	
3375 3380 3385	
gac tgt cct gaa ttt aga tgt cag cca ggc cga ttt cag tgt ggg	11067
Asp Cys Pro Glu Phe Arg Cys Gln Pro Gly Arg Phe Gln Cys Gly	
3390 3395 3400	
act gga ctc tgt gct cta cca gct ttc atc tgt gat gga gag aat	11112
Thr Gly Leu Cys Ala Leu Pro Ala Phe Ile Cys Asp Gly Glu Asn	
3405 3410 3415	
gat tgt gga gac aat tct gat gaa ctc aac tgt gac aca cat gtc	11157
Asp Cys Gly Asp Asn Ser Asp Glu Leu Asn Cys Asp Thr His Val	
3420 3425 3430	
tgc ctg tca ggt caa ttc aaa tgt acc aag aac cag aaa tgt atc	11202
Cys Leu Ser Gly Gln Phe Lys Cys Thr Lys Asn Gln Lys Cys Ile	
3435 3440 3445	

cca gta aac tta aga tgt aat ggg caa gat gac tgt ggt gat gag Pro Val Asn Leu Arg Cys Asn Gly Gln Asp Asp Cys Gly Asp Glu 3450 3455 3460	11247
gaa gat gaa aga gac tgt cct gaa aac agc tgt tct cca gac tat Glu Asp Glu Arg Asp Cys Pro Glu Asn Ser Cys Ser Pro Asp Tyr 3465 3470 3475	11292
ttc cag tgt aag act acg aag cat tgc att tcc aag ctg tgg gtt Phe Gln Cys Lys Thr Thr Lys His Cys Ile Ser Lys Leu Trp Val 3480 3485 3490	11337
tgt gac gag gat cca gac tgt gca gat gca tca gac gag gcc aac Cys Asp Glu Asp Pro Asp Cys Ala Asp Ala Ser Asp Glu Ala Asn 3495 3500 3505	11382
tgc gat aaa aag act tgt gga cct cat gaa ttc cag tgt aaa aac Cys Asp Lys Lys Thr Cys Gly Pro His Glu Phe Gln Cys Lys Asn 3510 3515 3520	11427
aac aac tgt att ccc gat cac tgg cgg tgt gat agc caa aat gac Asn Asn Cys Ile Pro Asp His Trp Arg Cys Asp Ser Gln Asn Asp 3525 3530 3535	11472
tgc agt gat aat tca gat gaa gaa aac tgt aag cca cag aca tgt Cys Ser Asp Asn Ser Asp Glu Glu Asn Cys Lys Pro Gln Thr Cys 3540 3545 3550	11517
aca ttg aaa gat ttc ctc tgt gcc aat ggg gac tgt gtt tct tca Thr Leu Lys Asp Phe Leu Cys Ala Asn Gly Asp Cys Val Ser Ser 3555 3560 3565	11562
agg ttt tgg tgt gat gga gat ttt gac tgt gca gat ggc tct gat Arg Phe Trp Cys Asp Gly Asp Phe Asp Cys Ala Asp Gly Ser Asp 3570 3575 3580	11607
gag aga aat tgt gag aca agt tgt tcc aaa gat cag ttc cgg tgt Glu Arg Asn Cys Glu Thr Ser Cys Ser Lys Asp Gln Phe Arg Cys 3585 3590 3595	11652
tcc aat ggt cag tgt ata cca gca aaa tgg aaa tgt gat ggc cat Ser Asn Gly Gln Cys Ile Pro Ala Lys Trp Lys Cys Asp Gly His 3600 3605 3610	11697
gaa gac tgc aaa tat ggg gaa gat gag aaa agc tgt gag cca gct Glu Asp Cys Lys Tyr Gly Glu Asp Glu Lys Ser Cys Glu Pro Ala 3615 3620 3625	11742
tct cct act tgc tca tca cgt gaa tat ata tgt gcc agt gat gga Ser Pro Thr Cys Ser Ser Arg Glu Tyr Ile Cys Ala Ser Asp Gly 3630 3635 3640	11787
tgt att tca gca tct ttg aaa tgt aat gga gaa tat gat tgt gct Cys Ile Ser Ala Ser Leu Lys Cys Asn Gly Glu Tyr Asp Cys Ala 3645 3650 3655	11832
gat ggt tca gat gag atg gac tgt gtg act gaa tgt aag gaa gat Asp Gly Ser Asp Glu Met Asp Cys Val Thr Glu Cys Lys Glu Asp 3660 3665 3670	11877
cag ttt cgg tgc aaa aat aaa gcc cac tgt att cca att aga tgg Gln Phe Arg Cys Lys Asn Lys Ala His Cys Ile Pro Ile Arg Trp 3675 3680 3685	11922

ctg tgt gat gga att cat gac tgt gtg gat ggc agt gat gaa gag	11967
Leu Cys Asp Gly Ile His Asp Cys Val Asp Gly Ser Asp Glu Glu	
3690 3695 3700	
aac tgt gaa aga gga gga aat ata tgt aga gct gat gag ttc ctt	12012
Asn Cys Glu Arg Gly Gly Asn Ile Cys Arg Ala Asp Glu Phe Leu	
3705 3710 3715	
tgc aat aat tct ctc tgc aaa cta cat ttc tgg gtg tgt gat gga	12057
Cys Asn Asn Ser Leu Cys Lys Leu His Phe Trp Val Cys Asp Gly	
3720 3725 3730	
gag gac gac tgt gga gac aac tct gat gaa gcc cct gat atg tgt	12102
Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Ala Pro Asp Met Cys	
3735 3740 3745	
gtc aaa ttt ctt tgt cca tcc acg aga cct cac aga tgc aga aat	12147
Val Lys Phe Leu Cys Pro Ser Thr Arg Pro His Arg Cys Arg Asn	
3750 3755 3760	
aac aga ata tgc cta cag tcg gag caa atg tgc aat ggg att gat	12192
Asn Arg Ile Cys Leu Gln Ser Glu Gln Met Cys Asn Gly Ile Asp	
3765 3770 3775	
gaa tgc ggt gac aat tca gat gaa gat cac tgt ggt ggt aag ctg	12237
Glu Cys Gly Asp Asn Ser Asp Glu Asp His Cys Gly Gly Lys Leu	
3780 3785 3790	
aca tat aaa gca agg cct tgt aaa aag gat gag ttt gct tgt agt	12282
Thr Tyr Lys Ala Arg Pro Cys Lys Lys Asp Glu Phe Ala Cys Ser	
3795 3800 3805	
aat aaa aaa tgc atc cct atg gat ctc cag tgt gat cga ctt gat	12327
Asn Lys Lys Cys Ile Pro Met Asp Leu Gln Cys Asp Arg Leu Asp	
3810 3815 3820	
gac tgc gga gat ggt tca gat gag caa gga tgc aga ata gct cct	12372
Asp Cys Gly Asp Gly Ser Asp Glu Gln Gly Cys Arg Ile Ala Pro	
3825 3830 3835	
act gaa tat acc tgt gaa gat aat gtg aat cca tgt gga gat gat	12417
Thr Glu Tyr Thr Cys Glu Asp Asn Val Asn Pro Cys Gly Asp Asp	
3840 3845 3850	
gca tat tgt aat caa ata aaa aca tct gtt ttc tgt cgc tgt aag	12462
Ala Tyr Cys Asn Gln Ile Lys Thr Ser Val Phe Cys Arg Cys Lys	
3855 3860 3865	
cct gga ttt cag aga aac atg aaa aac aga caa tgt gaa gac ctt	12507
Pro Gly Phe Gln Arg Asn Met Lys Asn Arg Gln Cys Glu Asp Leu	
3870 3875 3880	
aat gaa tgt ttg gtg ttt ggc aca tgt tcc cat caa tgt ata aat	12552
Asn Glu Cys Leu Val Phe Gly Thr Cys Ser His Gln Cys Ile Asn	
3885 3890 3895	
gtg gaa gga tca tat aaa tgt gtg tgt gac cag aat ttt caa gaa	12597
Val Glu Gly Ser Tyr Lys Cys Val Cys Asp Gln Asn Phe Gln Glu	
3900 3905 3910	
aga aat aac acc tgc ata gca gaa ggc tct gaa gat caa gtt ctc	12642
Arg Asn Asn Thr Cys Ile Ala Glu Gly Ser Glu Asp Gln Val Leu	
3915 3920 3925	

tac att gct aat gac act gat atc ctg ggt ttt ata tat cca ttc	12687
Tyr Ile Ala Asn Asp Thr Asp Ile Leu Gly Phe Ile Tyr Pro Phe	
3930 3935 3940	
aac tac agt ggc gat cat caa caa att tct cat att gaa cat aat	12732
Asn Tyr Ser Gly Asp His Gln Gln Ile Ser His Ile Glu His Asn	
3945 3950 3955	
tca aga ata aca ggg atg gat gta tat tat caa aga gat atg att	12777
Ser Arg Ile Thr Gly Met Asp Val Tyr Tyr Gln Arg Asp Met Ile	
3960 3965 3970	
att tgg agt act cag ttt aat cca ggc gga att ttc tac aaa agg	12822
Ile Trp Ser Thr Gln Phe Asn Pro Gly Gly Ile Phe Tyr Lys Arg	
3975 3980 3985	
atc cat ggc aga gaa aaa agg caa gca aac agt ggc ttg att tgt	12867
Ile His Gly Arg Glu Lys Arg Gln Ala Asn Ser Gly Leu Ile Cys	
3990 3995 4000	
cct gaa ttt aaa agg ccc agg gac att gca gtt gac tgg gtg gct	12912
Pro Glu Phe Lys Arg Pro Arg Asp Ile Ala Val Asp Trp Val Ala	
4005 4010 4015	
gga aac att tac tgg act gat cat tct aga atg cat tgg ttc agt	12957
Gly Asn Ile Tyr Trp Thr Asp His Ser Arg Met His Trp Phe Ser	
4020 4025 4030	
tac tac act act cac tgg acc agt ctg agg tac tct atc aac gta	13002
Tyr Tyr Thr Thr His Trp Thr Ser Leu Arg Tyr Ser Ile Asn Val	
4035 4040 4045	
ggg cag ctg aat ggc ccc aac tgc acc aga ctc tta aca aat atg	13047
Gly Gln Leu Asn Gly Pro Asn Cys Thr Arg Leu Leu Thr Asn Met	
4050 4055 4060	
gct gga gaa ccc tat gct att gca gta aat cct aaa aga ggg atg	13092
Ala Gly Glu Pro Tyr Ala Ile Ala Val Asn Pro Lys Arg Gly Met	
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Leu His Pro His Arg Ile Asp Ile Phe Glu Asp Tyr Ile Tyr Gly	
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Gly Ser Val	Glu Tyr Leu Ala Leu	Asn Ile Asp Lys Thr	Lys Gly	
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Val Leu Ile	Ser His Arg Tyr Lys	Gln Leu Asp Leu Pro	Asn Pro	
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Cys Leu Asp	Leu Ala Cys Glu Phe	Leu Cys Leu Leu Asn	Pro Ser	
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Gly Ala Thr	Cys Val Cys Pro Glu	Gly Lys Tyr Leu Ile	Asn Gly	
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Thr Cys Asn	Asp Asp Ser Leu Leu	Asp Asp Ser Cys Lys	Leu Thr	
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Cys Glu Asn	Gly Gly Arg Cys Ile	Leu Asn Glu Lys Gly	Asp Leu	
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Arg Cys His	Cys Trp Pro Ser Tyr	Ser Gly Glu Arg Cys	Glu Val	
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Asn His Cys	Ser Asn Tyr Cys Gln	Asn Gly Gly Thr Cys	Val Pro	
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Ser Val Leu	Gly Arg Pro Thr Cys	Ser Cys Ala Leu Gly	Phe Thr	
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Cys Gln Pro	Glu Tyr Thr Gly Asp	Arg Cys Gln Tyr Tyr	Val Cys	
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His His Tyr	Cys Val Asn Ser Glu	Ser Cys Thr Ile Gly	Asp Asp	
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Gly Ser Leu	Glu Cys Val Cys Pro	Thr Arg Tyr Glu Gly	Pro Lys	
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Cys Glu Val	Asp Lys Cys Val Arg	Cys His Gly Gly His	Cys Ile	
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Lys Ile Ala Ser Ser Cys Gln Leu	Cys Asp Gly Tyr Cys Tyr Asn	
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<400> 33

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35 40 45

Ser Gly Leu Leu Pro Ile Ala Arg Val Leu Thr Val Gly Ala Asp Arg
50 55 60

Asp Gln Gln Leu Cys Asp Pro Gly Glu Phe Leu Cys His Asp His Val
65 70 75 80

Thr Cys Val Ser Arg Ser Trp Leu Cys Asp Gly Asp Pro Asp Cys Pro
85 90 95

Asp Asp Ser Asp Glu Ser Leu Asp Thr Cys Pro Glu Glu Val Glu Ile
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Lys Cys Pro Leu Asn His Ile Ala Cys Leu Gly Thr Asn Lys Cys Val
115 120 125

His Leu Ser Gln Leu Cys Asn Gly Val Leu Asp Cys Pro Asp Gly Tyr
130 135 140

Asp Glu Gly Val His Cys Gln Glu Leu Leu Ser Asn Cys Gln Gln Leu
145 150 155 160

Asn Cys Gln Tyr Lys Cys Thr Met Val Arg Asn Ser Thr Arg Cys Tyr
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Cys Glu Asp Gly Phe Glu Ile Thr Glu Asp Gly Arg Ser Cys Lys Asp
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Gln Asp Glu Cys Ala Val Tyr Gly Thr Cys Ser Gln Thr Cys Arg Asn
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Thr His Gly Ser Tyr Thr Cys Ser Cys Val Glu Gly Tyr Leu Met Gln
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Pro Asp Asn Arg Ser Cys Lys Ala Lys Ile Glu Pro Thr Asp Arg Pro
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Pro Ile Leu Leu Ile Ala Asn Phe Glu Thr Ile Glu Val Phe Tyr Leu
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Asn Gly Ser Lys Met Ala Thr Leu Ser Ser Val Asn Gly Asn Glu Ile
260 265 270

His Thr Leu Asp Phe Ile Tyr Asn Glu Asp Val Ile Cys Trp Ile Glu
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Ser Arg Glu Ser Ser Asn Gln Leu Lys Cys Ile Gln Ile Thr Lys Ala
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Gly Gly Leu Thr Asp Glu Trp Thr Ile Asn Ile Leu Gln Ser Phe His
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Val Asp His Val Gly Asp Arg Ile Phe Val Cys Asn Ser Asn Gly Ser
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Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala Ala Leu Ala Leu Asp Leu
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Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met Ile Pro Ile Glu Asn Leu
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Val Asn Pro Arg Ala Leu Asp Phe His Ala Glu Thr Asn Tyr Ile Tyr
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Ile Ala Val Asp Trp Ile Gly Asn Asn Leu Tyr Trp Thr Asn Asp Gly
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Phe Asn Arg Gln Ile Phe Val Thr Ser Lys Met Leu Trp Pro Asn Gly
725 730 735

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865 870 875 880

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Ala Arg Trp Lys Cys Asp Gly Asp Asp Asp Cys Leu Asp Gly Ser Asp
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Glu Asp Ser Val Asn Cys Phe Asn His Ser Cys Pro Asp Asp Gln Phe
915 920 925

Lys Cys Gln Asn Asn Arg Cys Ile Pro Lys Arg Trp Leu Cys Asp Gly
930 935 940

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Leu	Ala	Gln	Leu	Gly	Thr	Cys	Ser	Lys	Arg	Asp	Gly	Arg	Asn	Pro
1835						1840					1845			
Thr	Ile	Leu	Arg	Asn	Lys	Thr	Ser	Gly	Val	Val	His	Met	Lys	Val
1850						1855					1860			
Tyr	Asp	Lys	Glu	Ala	Gln	Gln	Gly	Ser	Asn	Ser	Cys	Gln	Leu	Asn
1865						1870					1875			
Asn	Gly	Gly	Cys	Ser	Gln	Leu	Cys	Leu	Pro	Thr	Ser	Glu	Thr	Thr
1880						1885					1890			
Arg	Thr	Cys	Met	Cys	Thr	Val	Gly	Tyr	Tyr	Leu	Gln	Lys	Asn	Arg
1895						1900					1905			
Met	Ser	Cys	Gln	Gly	Ile	Glu	Ser	Phe	Leu	Met	Tyr	Ser	Val	His
1910						1915					1920			
Glu	Gly	Ile	Arg	Gly	Ile	Pro	Leu	Glu	Pro	Ser	Asp	Lys	Met	Asp
1925						1930					1935			
Ala	Leu	Met	Pro	Ile	Ser	Gly	Thr	Ser	Phe	Ala	Val	Gly	Ile	Asp
1940						1945					1950			
Phe	His	Ala	Glu	Asn	Asp	Thr	Ile	Tyr	Trp	Thr	Asp	Met	Gly	Phe
1955						1960					1965			
Asn	Lys	Ile	Ser	Arg	Ala	Lys	Arg	Asp	Gln	Thr	Trp	Lys	Glu	Asp
1970						1975					1980			

Ile	Ile	Thr	Asn	Gly	Leu	Gly	Arg	Val	Glu	Gly	Ile	Ala	Val	Asp
1985						1990					1995			
Trp	Ile	Ala	Gly	Asn	Ile	Tyr	Trp	Thr	Asp	His	Gly	Phe	Asn	Leu
2000						2005					2010			
Ile	Glu	Val	Ala	Arg	Leu	Asn	Gly	Ser	Phe	Arg	Tyr	Val	Ile	Ile
2015						2020					2025			
Ser	Gln	Gly	Leu	Asp	Gln	Pro	Arg	Ser	Ile	Ala	Val	His	Pro	Glu
2030						2035					2040			
Lys	Gly	Leu	Leu	Phe	Trp	Thr	Glu	Trp	Gly	Gln	Met	Pro	Cys	Ile
2045						2050					2055			
Gly	Lys	Ala	Arg	Leu	Asp	Gly	Ser	Glu	Lys	Val	Val	Leu	Val	Ser
2060						2065					2070			
Met	Gly	Ile	Ala	Trp	Pro	Asn	Gly	Ile	Ser	Ile	Asp	Tyr	Glu	Glu
2075						2080					2085			
Asn	Lys	Leu	Tyr	Trp	Cys	Asp	Ala	Arg	Thr	Asp	Lys	Ile	Glu	Arg
2090						2095					2100			
Ile	Asp	Leu	Glu	Thr	Gly	Gly	Asn	Arg	Glu	Met	Val	Leu	Ser	Gly
2105						2110					2115			
Ser	Asn	Val	Asp	Met	Phe	Ser	Val	Ala	Val	Phe	Gly	Ala	Tyr	Ile
2120						2125					2130			
Tyr	Trp	Ser	Asp	Arg	Ala	His	Ala	Asn	Gly	Ser	Val	Arg	Arg	Gly
2135						2140					2145			
His	Lys	Asn	Asp	Ala	Thr	Glu	Thr	Ile	Thr	Met	Arg	Thr	Gly	Leu
2150						2155					2160			
Gly	Val	Asn	Leu	Lys	Glu	Val	Lys	Ile	Phe	Asn	Arg	Val	Arg	Glu
2165						2170					2175			
Lys	Gly	Thr	Asn	Val	Cys	Ala	Arg	Asp	Asn	Gly	Gly	Cys	Lys	Gln
2180						2185					2190			
Leu	Cys	Leu	Tyr	Arg	Gly	Asn	Ser	Arg	Arg	Thr	Cys	Ala	Cys	Ala
2195						2200					2205			
His	Gly	Tyr	Leu	Ala	Glu	Asp	Gly	Val	Thr	Cys	Leu	Arg	His	Glu
2210						2215					2220			

Gly	Tyr	Leu	Leu	Tyr	Ser	Gly	Arg	Thr	Ile	Leu	Lys	Ser	Ile	His
2225						2230					2235			
Leu	Ser	Asp	Glu	Thr	Asn	Leu	Asn	Ser	Pro	Ile	Arg	Pro	Tyr	Glu
2240						2245					2250			
Asn	Pro	Arg	Tyr	Phe	Lys	Asn	Val	Ile	Ala	Leu	Ala	Phe	Asp	Tyr
2255						2260					2265			
Asn	Gln	Arg	Arg	Lys	Gly	Thr	Asn	Arg	Ile	Phe	Tyr	Ser	Asp	Ala
2270						2275					2280			
His	Phe	Gly	Asn	Ile	Gln	Leu	Ile	Lys	Asp	Asn	Trp	Glu	Asp	Arg
2285						2290					2295			
Gln	Val	Ile	Val	Glu	Asn	Val	Gly	Ser	Val	Glu	Gly	Leu	Ala	Tyr
2300						2305					2310			
His	Arg	Ala	Trp	Asp	Thr	Leu	Tyr	Trp	Thr	Ser	Ser	Thr	Thr	Ser
2315						2320					2325			
Ser	Ile	Thr	Arg	His	Thr	Val	Asp	Gln	Thr	Arg	Pro	Gly	Ala	Phe
2330						2335					2340			
Asp	Arg	Glu	Ala	Val	Ile	Thr	Met	Ser	Glu	Asp	Asp	His	Pro	His
2345						2350					2355			
Val	Leu	Ala	Leu	Asp	Glu	Cys	Gln	Asn	Leu	Met	Phe	Trp	Thr	Asn
2360						2365					2370			
Trp	Asn	Glu	Gln	His	Pro	Ser	Ile	Met	Arg	Ser	Thr	Leu	Thr	Gly
2375						2380					2385			
Lys	Asn	Ala	Gln	Val	Val	Val	Ser	Thr	Asp	Ile	Leu	Thr	Pro	Asn
2390						2395					2400			
Gly	Leu	Thr	Ile	Asp	Tyr	Arg	Ala	Glu	Lys	Leu	Tyr	Phe	Ser	Asp
2405						2410					2415			
Gly	Ser	Leu	Gly	Lys	Ile	Glu	Arg	Cys	Glu	Tyr	Asp	Gly	Ser	Gln
2420						2425					2430			
Arg	His	Val	Ile	Val	Lys	Ser	Gly	Pro	Gly	Thr	Phe	Leu	Ser	Leu
2435						2440					2445			
Ala	Val	Tyr	Asp	Asn	Tyr	Ile	Phe	Trp	Ser	Asp	Trp	Gly	Arg	Arg
2450						2455					2460			

Ala	Ile	Leu	Arg	Ser	Asn	Lys	Tyr	Thr	Gly	Gly	Asp	Thr	Lys	Ile
2465						2470					2475			
Leu	Arg	Ser	Asp	Ile	Pro	His	Gln	Pro	Met	Gly	Ile	Ile	Ala	Val
2480						2485					2490			
Ala	Asn	Asp	Thr	Asn	Ser	Cys	Glu	Leu	Ser	Pro	Cys	Ala	Leu	Leu
2495						2500					2505			
Asn	Gly	Gly	Cys	His	Asp	Leu	Cys	Leu	Leu	Thr	Pro	Asn	Gly	Arg
2510						2515					2520			
Val	Asn	Cys	Ser	Cys	Arg	Gly	Asp	Arg	Ile	Leu	Leu	Glu	Asp	Asn
2525						2530					2535			
Arg	Cys	Val	Thr	Lys	Asn	Ser	Ser	Cys	Asn	Ala	Tyr	Ser	Glu	Phe
2540						2545					2550			
Glu	Cys	Gly	Asn	Gly	Glu	Cys	Ile	Asp	Tyr	Gln	Leu	Thr	Cys	Asp
2555						2560					2565			
Gly	Ile	Pro	His	Cys	Lys	Asp	Lys	Ser	Asp	Glu	Lys	Leu	Leu	Tyr
2570						2575					2580			
Cys	Glu	Asn	Arg	Ser	Cys	Arg	Arg	Gly	Phe	Lys	Pro	Cys	Tyr	Asn
2585						2590					2595			
Arg	Arg	Cys	Ile	Pro	His	Gly	Lys	Leu	Cys	Asp	Gly	Glu	Asn	Asp
2600						2605					2610			
Cys	Gly	Asp	Asn	Ser	Asp	Glu	Leu	Asp	Cys	Lys	Val	Ser	Thr	Cys
2615						2620					2625			
Ala	Thr	Val	Glu	Phe	Arg	Cys	Ala	Asp	Gly	Thr	Cys	Ile	Pro	Arg
2630						2635					2640			
Ser	Ala	Arg	Cys	Asn	Gln	Asn	Ile	Asp	Cys	Ala	Asp	Ala	Ser	Asp
2645						2650					2655			
Glu	Lys	Asn	Cys	Asn	Asn	Thr	Asp	Cys	Thr	His	Phe	Tyr	Lys	Leu
2660						2665					2670			
Gly	Val	Lys	Thr	Thr	Gly	Phe	Ile	Arg	Cys	Asn	Ser	Thr	Ser	Leu
2675						2680					2685			
Cys	Val	Leu	Pro	Thr	Trp	Ile	Cys	Asp	Gly	Ser	Asn	Asp	Cys	Gly
2690						2695					2700			

Asp Tyr	Ser Asp Glu Leu Lys	Cys Pro Val Gln Asn	Lys His Lys
2705	2710	2715	
Cys Glu	Glu Asn Tyr Phe Ser	Cys Pro Ser Gly Arg	Cys Ile Leu
2720	2725	2730	
Asn Thr	Trp Ile Cys Asp Gly	Gln Lys Asp Cys Glu	Asp Gly Arg
2735	2740	2745	
Asp Glu	Phe His Cys Asp Ser	Ser Cys Ser Trp Asn	Gln Phe Ala
2750	2755	2760	
Cys Ser	Ala Gln Lys Cys Ile	Ser Lys His Trp Ile	Cys Asp Gly
2765	2770	2775	
Glu Asp	Asp Cys Gly Asp Gly	Leu Asp Glu Ser Asp	Ser Ile Cys
2780	2785	2790	
Gly Ala	Ile Thr Cys Ala Ala	Asp Met Phe Ser Cys	Gln Gly Ser
2795	2800	2805	
Arg Ala	Cys Val Pro Arg His	Trp Leu Cys Asp Gly	Glu Arg Asp
2810	2815	2820	
Cys Pro	Asp Gly Ser Asp Glu	Leu Ser Thr Ala Gly	Cys Ala Pro
2825	2830	2835	
Asn Asn	Thr Cys Asp Glu Asn	Ala Phe Met Cys His	Asn Lys Val
2840	2845	2850	
Cys Ile	Pro Lys Gln Phe Val	Cys Asp His Asp Asp	Asp Cys Gly
2855	2860	2865	
Asp Gly	Ser Asp Glu Ser Pro	Gln Cys Gly Tyr Arg	Gln Cys Gly
2870	2875	2880	
Thr Glu	Glu Phe Ser Cys Ala	Asp Gly Arg Cys Leu	Leu Asn Thr
2885	2890	2895	
Gln Trp	Gln Cys Asp Gly Asp	Phe Asp Cys Pro Asp	His Ser Asp
2900	2905	2910	
Glu Ala	Pro Leu Asn Pro Lys	Cys Lys Ser Ala Glu	Gln Ser Cys
2915	2920	2925	
Asn Ser	Ser Phe Phe Met Cys	Lys Asn Gly Arg Cys	Ile Pro Ser
2930	2935	2940	

Gly Gly	Leu Cys Asp Asn Lys	Asp Asp Cys Gly Asp	Gly Ser Asp
2945	2950	2955	
Glu Arg	Asn Cys His Ile Asn	Glu Cys Leu Ser Lys	Lys Val Ser
2960	2965	2970	
Gly Cys	Ser Gln Asp Cys Gln	Asp Leu Pro Val Ser	Tyr Lys Cys
2975	2980	2985	
Lys Cys	Trp Pro Gly Phe Gln	Leu Lys Asp Asp Gly	Lys Thr Cys
2990	2995	3000	
Val Asp	Ile Asp Glu Cys Ser	Ser Gly Phe Pro Cys	Ser Gln Gln
3005	3010	3015	
Cys Ile	Asn Thr Tyr Gly Thr	Tyr Lys Cys Leu Cys	Thr Asp Gly
3020	3025	3030	
Tyr Glu	Ile Gln Pro Asp Asn	Pro Asn Gly Cys Lys	Ser Leu Ser
3035	3040	3045	
Asp Glu	Glu Pro Phe Leu Ile	Leu Ala Asp His His	Glu Ile Arg
3050	3055	3060	
Lys Ile	Ser Thr Asp Gly Ser	Asn Tyr Thr Leu Leu	Lys Gln Gly
3065	3070	3075	
Leu Asn	Asn Val Ile Ala Ile	Asp Phe Asp Tyr Arg	Glu Glu Phe
3080	3085	3090	
Ile Tyr	Trp Ile Asp Ser Ser	Arg Pro Asn Gly Ser	Arg Ile Asn
3095	3100	3105	
Arg Met	Cys Leu Asn Gly Ser	Asp Ile Lys Val Val	His Asn Thr
3110	3115	3120	
Ala Val	Pro Asn Ala Leu Ala	Val Asp Trp Ile Gly	Lys Asn Leu
3125	3130	3135	
Tyr Trp	Ser Asp Thr Glu Lys	Arg Ile Ile Glu Val	Ser Lys Leu
3140	3145	3150	
Asn Gly	Leu Tyr Pro Thr Ile	Leu Val Ser Lys Arg	Leu Lys Phe
3155	3160	3165	
Pro Arg	Asp Leu Ser Leu Asp	Pro Gln Ala Gly Tyr	Leu Tyr Trp
3170	3175	3180	

Ile	Asp	Cys	Cys	Glu	Tyr	Pro	His	Ile	Gly	Arg	Val	Gly	Met	Asp
3185						3190					3195			
Gly	Thr	Asn	Gln	Ser	Val	Val	Ile	Glu	Thr	Lys	Ile	Ser	Arg	Pro
3200						3205					3210			
Met	Ala	Leu	Thr	Ile	Asp	Tyr	Val	Asn	Arg	Arg	Leu	Tyr	Trp	Ala
3215						3220					3225			
Asp	Glu	Asn	His	Ile	Glu	Phe	Ser	Asn	Met	Asp	Gly	Ser	His	Arg
3230						3235					3240			
His	Lys	Val	Pro	Asn	Gln	Asp	Ile	Pro	Gly	Val	Ile	Ala	Leu	Thr
3245						3250					3255			
Leu	Phe	Glu	Asp	Tyr	Ile	Tyr	Trp	Thr	Asp	Gly	Lys	Thr	Lys	Ser
3260						3265					3270			
Leu	Ser	Arg	Ala	His	Lys	Thr	Ser	Gly	Ala	Asp	Arg	Leu	Ser	Leu
3275						3280					3285			
Ile	Tyr	Ser	Trp	His	Ala	Ile	Thr	Asp	Ile	Gln	Val	Tyr	His	Ser
3290						3295					3300			
Tyr	Arg	Gln	Pro	Asp	Val	Ser	Lys	His	Leu	Cys	Met	Ile	Asn	Asn
3305						3310					3315			
Gly	Gly	Cys	Ser	His	Leu	Cys	Leu	Leu	Ala	Pro	Gly	Lys	Thr	His
3320						3325					3330			
Thr	Cys	Ala	Cys	Pro	Thr	Asn	Phe	Tyr	Leu	Ala	Ala	Asp	Asn	Arg
3335						3340					3345			
Thr	Cys	Leu	Ser	Asn	Cys	Thr	Ala	Ser	Gln	Phe	Arg	Cys	Lys	Thr
3350						3355					3360			
Asp	Lys	Cys	Ile	Pro	Phe	Trp	Trp	Lys	Cys	Asp	Thr	Val	Asp	Asp
3365						3370					3375			
Cys	Gly	Asp	Gly	Ser	Asp	Glu	Pro	Asp	Asp	Cys	Pro	Glu	Phe	Arg
3380						3385					3390			
Cys	Gln	Pro	Gly	Arg	Phe	Gln	Cys	Gly	Thr	Gly	Leu	Cys	Ala	Leu
3395						3400					3405			
Pro	Ala	Phe	Ile	Cys	Asp	Gly	Glu	Asn	Asp	Cys	Gly	Asp	Asn	Ser
3410						3415					3420			

Asp Glu Leu Asn Cys Asp Thr His Val Cys Leu Ser Gly Gln Phe
3425 3430 3435

Lys Cys Thr Lys Asn Gln Lys Cys Ile Pro Val Asn Leu Arg Cys
3440 3445 3450

Asn Gly Gln Asp Asp Cys Gly Asp Glu Glu Asp Glu Arg Asp Cys
3455 3460 3465

Pro Glu Asn Ser Cys Ser Pro Asp Tyr Phe Gln Cys Lys Thr Thr
3470 3475 3480

Lys His Cys Ile Ser Lys Leu Trp Val Cys Asp Glu Asp Pro Asp
3485 3490 3495

Cys Ala Asp Ala Ser Asp Glu Ala Asn Cys Asp Lys Lys Thr Cys
3500 3505 3510

Gly Pro His Glu Phe Gln Cys Lys Asn Asn Asn Cys Ile Pro Asp
3515 3520 3525

His Trp Arg Cys Asp Ser Gln Asn Asp Cys Ser Asp Asn Ser Asp
3530 3535 3540

Glu Glu Asn Cys Lys Pro Gln Thr Cys Thr Leu Lys Asp Phe Leu
3545 3550 3555

Cys Ala Asn Gly Asp Cys Val Ser Ser Arg Phe Trp Cys Asp Gly
3560 3565 3570

Asp Phe Asp Cys Ala Asp Gly Ser Asp Glu Arg Asn Cys Glu Thr
3575 3580 3585

Ser Cys Ser Lys Asp Gln Phe Arg Cys Ser Asn Gly Gln Cys Ile
3590 3595 3600

Pro Ala Lys Trp Lys Cys Asp Gly His Glu Asp Cys Lys Tyr Gly
3605 3610 3615

Glu Asp Glu Lys Ser Cys Glu Pro Ala Ser Pro Thr Cys Ser Ser
3620 3625 3630

Arg Glu Tyr Ile Cys Ala Ser Asp Gly Cys Ile Ser Ala Ser Leu
3635 3640 3645

Lys Cys Asn Gly Glu Tyr Asp Cys Ala Asp Gly Ser Asp Glu Met
3650 3655 3660

Asp Cys	Val Thr Glu Cys Lys	Glu Asp Gln Phe Arg	Cys Lys Asn
3665	3670	3675	
Lys Ala	His Cys Ile Pro Ile	Arg Trp Leu Cys Asp	Gly Ile His
3680	3685	3690	
Asp Cys	Val Asp Gly Ser Asp	Glu Glu Asn Cys Glu	Arg Gly Gly
3695	3700	3705	
Asn Ile	Cys Arg Ala Asp Glu	Phe Leu Cys Asn Asn	Ser Leu Cys
3710	3715	3720	
Lys Leu	His Phe Trp Val Cys	Asp Gly Glu Asp Asp	Cys Gly Asp
3725	3730	3735	
Asn Ser	Asp Glu Ala Pro Asp	Met Cys Val Lys Phe	Leu Cys Pro
3740	3745	3750	
Ser Thr	Arg Pro His Arg Cys	Arg Asn Asn Arg Ile	Cys Leu Gln
3755	3760	3765	
Ser Glu	Gln Met Cys Asn Gly	Ile Asp Glu Cys Gly	Asp Asn Ser
3770	3775	3780	
Asp Glu	Asp His Cys Gly Gly	Lys Leu Thr Tyr Lys	Ala Arg Pro
3785	3790	3795	
Cys Lys	Lys Asp Glu Phe Ala	Cys Ser Asn Lys Lys	Cys Ile Pro
3800	3805	3810	
Met Asp	Leu Gln Cys Asp Arg	Leu Asp Asp Cys Gly	Asp Gly Ser
3815	3820	3825	
Asp Glu	Gln Gly Cys Arg Ile	Ala Pro Thr Glu Tyr	Thr Cys Glu
3830	3835	3840	
Asp Asn	Val Asn Pro Cys Gly	Asp Asp Ala Tyr Cys	Asn Gln Ile
3845	3850	3855	
Lys Thr	Ser Val Phe Cys Arg	Cys Lys Pro Gly Phe	Gln Arg Asn
3860	3865	3870	
Met Lys	Asn Arg Gln Cys Glu	Asp Leu Asn Glu Cys	Leu Val Phe
3875	3880	3885	
Gly Thr	Cys Ser His Gln Cys	Ile Asn Val Glu Gly	Ser Tyr Lys
3890	3895	3900	

Cys Val	Cys Asp Gln Asn Phe	Gln Glu Arg Asn Asn	Thr Cys Ile
3905	3910	3915	
Ala Glu	Gly Ser Glu Asp Gln	Val Leu Tyr Ile Ala	Asn Asp Thr
3920	3925	3930	
Asp Ile	Leu Gly Phe Ile Tyr	Pro Phe Asn Tyr Ser	Gly Asp His
3935	3940	3945	
Gln Gln	Ile Ser His Ile Glu	His Asn Ser Arg Ile	Thr Gly Met
3950	3955	3960	
Asp Val	Tyr Tyr Gln Arg Asp	Met Ile Ile Trp Ser	Thr Gln Phe
3965	3970	3975	
Asn Pro	Gly Gly Ile Phe Tyr	Lys Arg Ile His Gly	Arg Glu Lys
3980	3985	3990	
Arg Gln	Ala Asn Ser Gly Leu	Ile Cys Pro Glu Phe	Lys Arg Pro
3995	4000	4005	
Arg Asp	Ile Ala Val Asp Trp	Val Ala Gly Asn Ile	Tyr Trp Thr
4010	4015	4020	
Asp His	Ser Arg Met His Trp	Phe Ser Tyr Tyr Thr	Thr His Trp
4025	4030	4035	
Thr Ser	Leu Arg Tyr Ser Ile	Asn Val Gly Gln Leu	Asn Gly Pro
4040	4045	4050	
Asn Cys	Thr Arg Leu Leu Thr	Asn Met Ala Gly Glu	Pro Tyr Ala
4055	4060	4065	
Ile Ala	Val Asn Pro Lys Arg	Gly Met Met Tyr Trp	Thr Val Val
4070	4075	4080	
Gly Asp	His Ser His Ile Glu	Glu Ala Ala Met Asp	Gly Thr Leu
4085	4090	4095	
Arg Arg	Ile Leu Val Gln Lys	Asn Leu Gln Arg Pro	Thr Gly Leu
4100	4105	4110	
Ala Val	Asp Tyr Phe Ser Glu	Arg Ile Tyr Trp Ala	Asp Phe Glu
4115	4120	4125	
Leu Ser	Ile Ile Gly Ser Val	Leu Tyr Asp Gly Ser	Asn Ser Val
4130	4135	4140	

Val	Ser	Val	Ser	Ser	Lys	Gln	Gly	Leu	Leu	His	Pro	His	Arg	Ile
4145						4150					4155			
Asp	Ile	Phe	Glu	Asp	Tyr	Ile	Tyr	Gly	Ala	Gly	Pro	Lys	Asn	Gly
4160						4165					4170			
Val	Phe	Arg	Val	Gln	Lys	Phe	Gly	His	Gly	Ser	Val	Glu	Tyr	Leu
4175						4180					4185			
Ala	Leu	Asn	Ile	Asp	Lys	Thr	Lys	Gly	Val	Leu	Ile	Ser	His	Arg
4190						4195					4200			
Tyr	Lys	Gln	Leu	Asp	Leu	Pro	Asn	Pro	Cys	Leu	Asp	Leu	Ala	Cys
4205						4210					4215			
Glu	Phe	Leu	Cys	Leu	Leu	Asn	Pro	Ser	Gly	Ala	Thr	Cys	Val	Cys
4220						4225					4230			
Pro	Glu	Gly	Lys	Tyr	Leu	Ile	Asn	Gly	Thr	Cys	Asn	Asp	Asp	Ser
4235						4240					4245			
Leu	Leu	Asp	Asp	Ser	Cys	Lys	Leu	Thr	Cys	Glu	Asn	Gly	Gly	Arg
4250						4255					4260			
Cys	Ile	Leu	Asn	Glu	Lys	Gly	Asp	Leu	Arg	Cys	His	Cys	Trp	Pro
4265						4270					4275			
Ser	Tyr	Ser	Gly	Glu	Arg	Cys	Glu	Val	Asn	His	Cys	Ser	Asn	Tyr
4280						4285					4290			
Cys	Gln	Asn	Gly	Gly	Thr	Cys	Val	Pro	Ser	Val	Leu	Gly	Arg	Pro
4295						4300					4305			
Thr	Cys	Ser	Cys	Ala	Leu	Gly	Phe	Thr	Gly	Pro	Asn	Cys	Gly	Lys
4310						4315					4320			
Thr	Val	Cys	Glu	Asp	Phe	Cys	Gln	Asn	Gly	Gly	Thr	Cys	Ile	Val
4325						4330					4335			
Thr	Ala	Gly	Asn	Gln	Pro	Tyr	Cys	His	Cys	Gln	Pro	Glu	Tyr	Thr
4340						4345					4350			
Gly	Asp	Arg	Cys	Gln	Tyr	Tyr	Val	Cys	His	His	Tyr	Cys	Val	Asn
4355						4360					4365			
Ser	Glu	Ser	Cys	Thr	Ile	Gly	Asp	Asp	Gly	Ser	Leu	Glu	Cys	Val
4370						4375					4380			

Cys	Pro	Thr	Arg	Tyr	Glu	Gly	Pro	Lys	Cys	Glu	Val	Asp	Lys	Cys
4385						4390					4395			
Val	Arg	Cys	His	Gly	Gly	His	Cys	Ile	Ile	Asn	Lys	Asp	Ser	Glu
4400						4405					4410			
Asp	Ile	Phe	Cys	Asn	Cys	Thr	Asn	Gly	Lys	Ile	Ala	Ser	Ser	Cys
4415						4420					4425			
Gln	Leu	Cys	Asp	Gly	Tyr	Cys	Tyr	Asn	Gly	Gly	Thr	Cys	Gln	Leu
4430						4435					4440			
Asp	Pro	Glu	Thr	Asn	Val	Pro	Val	Cys	Leu	Cys	Ser	Thr	Asn	Trp
4445						4450					4455			
Ser	Gly	Thr	Gln	Cys	Glu	Arg	Pro	Ala	Pro	Lys	Ser	Ser	Lys	Ser
4460						4465					4470			
Asp	His	Ile	Ser	Thr	Arg	Ser	Ile	Ala	Ile	Ile	Val	Pro	Leu	Val
4475						4480					4485			
Leu	Leu	Val	Thr	Leu	Ile	Thr	Thr	Leu	Val	Ile	Gly	Leu	Val	Leu
4490						4495					4500			
Cys	Lys	Arg	Lys	Arg	Arg	Thr	Lys	Thr	Ile	Arg	Arg	Gln	Pro	Ile
4505						4510					4515			
Ile	Asn	Gly	Gly	Ile	Asn	Val	Glu	Ile	Gly	Asn	Pro	Ser	Tyr	Asn
4520						4525					4530			
Met	Tyr	Glu	Val	Asp	His	Asp	His	Asn	Asp	Gly	Gly	Leu	Leu	Asp
4535						4540					4545			
Pro	Gly	Phe	Met	Ile	Asp	Pro	Thr	Lys	Ala	Arg	Tyr	Ile	Gly	Gly
4550						4555					4560			
Gly	Pro	Ser	Ala	Phe	Lys	Leu	Pro	His	Thr	Ala	Pro	Pro	Ile	Tyr
4565						4570					4575			
Leu	Asn	Ser	Asp	Leu	Lys	Gly	Pro	Leu	Thr	Ala	Gly	Pro	Thr	Asn
4580						4585					4590			
Tyr	Ser	Asn	Pro	Val	Tyr	Ala	Lys	Leu	Tyr	Met	Asp	Gly	Gln	Asn
4595						4600					4605			
Cys	Arg	Asn	Ser	Leu	Gly	Ser	Val	Asp	Glu	Arg	Lys	Glu	Leu	Leu
4610						4615					4620			

Pro Lys Lys Ile Glu Ile Gly Ile Arg Glu Thr Val Ala
4625 4630 4635

<210> 34
<211> 2242
<212> DNA
<213> Homo sapiens

<220>
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<222> (2223)
<223> n = a, c, g, or t

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cgaccagtgg ccctgaccct gctgactttg tgcttggtgc tgctgatagg gctggcagcc 300
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caaatggaag aaagattagg aaatacgtcc caagagttgc aatctcttca agtccagaat 420
ataaagcttg caggaagtct gcagcatgtg gctgaaaaac tctgtcgtga gctgtataac 480
aaagctggag cacacaggtg cagcccttgt acagaacaat ggaaatggca tggagacaat 540
tgctaccagt tctataaaga cagcaaaagt tgggaggact gtaaatatatt ctgccttagt 600
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ccagcaaata cacaaggaat tctttttgtt tgtttcagtt catactagtc ccttcccaat 1440

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agaaaacagt tttaacgttt tcctaaaatg aaatcttttg aggtgagctt atggcatcaa 2040
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<210> 35
<211> 280
<212> PRT
<213> Homo sapiens

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20          25          30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
35          40          45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
50          55          60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
65          70          75          80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
85          90          95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100         105         110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
115         120         125

Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His
130         135         140

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Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp
 145 150 155 160

Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn
 165 170 175

Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe
 180 185 190

Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala
 195 200 205

Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile
 210 215 220

Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
 225 230 235 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val
 245 250 255

Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro
 260 265 270

Pro Glu Thr Leu Gly Glu Gly Asp
 275 280

<210> 36
 <211> 2323
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (2304)
 <223> n = a, c, g, or t

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 acgagggaca tgctggatga tgatggggac accaccatga gcctgcattc tcaagcctct 180
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 caaatggaag aaagattagg aaatacgtcc caagagttgc aatctcttca agtccagaat 420
 ataaagcttg caggaagtct gcagcatgtg gctgaaaaac tctgtcgtga gctgtataac 480
 aaagctggag gctatacaag aaacatggtg ccagcatctg cttcttctga gagcctcagg 540
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 tggaaatggc atggagacaa ttgctaccag ttctataaag acagcaaaag ttgggaggac 660
 tgtaaataatt tctgccttag tgaaaactct accatgctga agataaacia acaagaagac 720
 ctggaatttg ccgcgtctca gagctactct gagtttttct actcttattg gacagggcctt 780

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aatgggatga tcttctcaaa ggactgcaaa gaattgaagc gttgtgtctg tgagagaagg 960
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<210> 37
<211> 307
<212> PRT
<213> Homo sapiens

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<400> 37
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1          5          10          15

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		35					40					45			
Pro	Val	Ala	Leu	Thr	Leu	Leu	Thr	Leu	Cys	Leu	Val	Leu	Leu	Ile	Gly
	50					55					60				
Leu	Ala	Ala	Leu	Gly	Leu	Leu	Phe	Phe	Gln	Tyr	Tyr	Gln	Leu	Ser	Asn
65					70					75					80
Thr	Gly	Gln	Asp	Thr	Ile	Ser	Gln	Met	Glu	Glu	Arg	Leu	Gly	Asn	Thr
				85					90					95	
Ser	Gln	Glu	Leu	Gln	Ser	Leu	Gln	Val	Gln	Asn	Ile	Lys	Leu	Ala	Gly
			100					105					110		
Ser	Leu	Gln	His	Val	Ala	Glu	Lys	Leu	Cys	Arg	Glu	Leu	Tyr	Asn	Lys
		115					120					125			
Ala	Gly	Gly	Tyr	Thr	Arg	Asn	Met	Val	Pro	Ala	Ser	Ala	Ser	Ser	Glu
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Ser	Leu	Arg	Gln	Leu	Pro	His	Met	Gly	Glu	Ser	Ala	Ala	Ala	His	Arg
145					150					155					160
Cys	Ser	Pro	Cys	Thr	Glu	Gln	Trp	Lys	Trp	His	Gly	Asp	Asn	Cys	Tyr
				165					170					175	
Gln	Phe	Tyr	Lys	Asp	Ser	Lys	Ser	Trp	Glu	Asp	Cys	Lys	Tyr	Phe	Cys
			180					185					190		
Leu	Ser	Glu	Asn	Ser	Thr	Met	Leu	Lys	Ile	Asn	Lys	Gln	Glu	Asp	Leu
		195					200					205			
Glu	Phe	Ala	Ala	Ser	Gln	Ser	Tyr	Ser	Glu	Phe	Phe	Tyr	Ser	Tyr	Trp
	210					215					220				
Thr	Gly	Leu	Leu	Arg	Pro	Asp	Ser	Gly	Lys	Ala	Trp	Leu	Trp	Met	Asp
225					230					235					240
Gly	Thr	Pro	Phe	Thr	Ser	Glu	Leu	Phe	His	Ile	Ile	Ile	Asp	Val	Thr
				245					250					255	
Ser	Pro	Arg	Ser	Arg	Asp	Cys	Val	Ala	Ile	Leu	Asn	Gly	Met	Ile	Phe
			260					265					270		
Ser	Lys	Asp	Cys	Lys	Glu	Leu	Lys	Arg	Cys	Val	Cys	Glu	Arg	Arg	Ala
		275					280					285			
Gly	Met	Val	Lys	Pro	Glu	Ser	Leu	His	Val	Pro	Pro	Glu	Thr	Leu	Gly
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Glu	Gly	Asp													
305															

<210> 38
 <211> 2714
 <212> DNA
 <213> Homo sapiens

<400> 38
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<210> 39
 <211> 769
 <212> PRT
 <213> Homo sapiens

<400> 39
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 20 25 30
 Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
 35 40 45
 Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
 50 55 60
 Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
 65 70 75 80
 Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
 85 90 95
 Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
 100 105 110
 Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
 115 120 125
 Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
 130 135 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
 145 150 155 160
 Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
 165 170 175
 Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
 180 185 190
 Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
 195 200 205
 Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
 210 215 220
 Val Asn Ala Ala Phe Tyr Arg Lys Leu Arg Lys Arg Ala Ala Lys Val
 225 230 235 240
 Ser Ala Arg His Pro Lys Pro Leu Gly Arg Leu Leu Ala Gln Arg Gln
 245 250 255
 Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala
 260 265 270
 His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala
 275 280 285
 Arg Cys Pro Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro
 290 295 300
 Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro
 305 310 315 320
 Gln Gly Glu Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu
 325 330 335
 Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp
 340 345 350
 Arg Lys Trp Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly
 355 360 365
 Phe Gly Ser Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly
 370 375 380
 Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu
 385 390 395 400
 Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser
 405 410 415
 His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala
 420 425 430
 Glu Thr Arg Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg
 435 440 445
 Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile
 450 455 460
 Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln
 465 470 475 480

Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp
 485 490 495
 Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr
 500 505 510
 Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile
 515 520 525
 Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser
 530 535 540
 Glu Thr Ala Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr
 545 550 555 560
 Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu
 565 570 575
 Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly
 580 585 590
 His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg
 595 600 605
 Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu
 610 615 620
 Cys His Gly His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile
 625 630 635 640
 Leu Thr Pro Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe
 645 650 655
 Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu
 660 665 670
 Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu
 675 680 685
 Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys
 690 695 700
 Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val
 705 710 715 720
 Ala Glu Ser Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr
 725 730 735
 Asp Gly His Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe
 740 745 750
 Ser Glu Glu Ala His Arg Arg Phe Glu Arg Ser Pro Gly Gln Thr Ser
 755 760 765

Thr

<210> 40
 <211> 1877
 <212> DNA
 <213> Homo sapiens

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aaggttctga gcaagctgca ggcccgtctg gatgacctgt gggaagacat cactcacagc 1200
cttcatgacc agggccacag ccattctggg gacctctgag gatctacctg ccaggccca 1260
ttcccagctc cttgtctggg gagccttggc tctgagcctc tagcatggtt cagtcttga 1320
aagtggcctg ttgggtggag ggtggaaggt cctgtgcagg acagggaggc caccaaaggg 1380
gctgctgtct cctgcacatc cagcctcctg cgactcccca atctggatgc attacattca 1440
ccaggctttg caaaccacgc ctcccagtgc tcatttggga atgctcatga gttactccat 1500
tcaagggtga gggagtaggg agggagaggc accatgcatg tgggtgatta tctgcaagcc 1560
tgtttgccgt gatgctggaa gcctgtgcca ctacatcctg gagtctgaca ctgagcccct 1620
gcgagtgacc gtgagcacac agttccgtag cggggcccat acgagactcg acgcgcgcgc 1680
accacgaggt ccgaggggag gacactcgac ggacacgagt gacgggaaat gtgcatctac 1740
actagcgcgc gacagctaga gcgatgacgg cgaggacgtc tcgcagccta ccagcaacgc 1800
gaagacgtgc ctcccgccgt cgtatggatt aacaagctcc aagtaggggtg tacaacgccg 1860

cagcatgaac tcccagg

<210> 41
<211> 400
<212> PRT
<213> Homo sapiens

<400> 41
Met Asn Lys Lys Lys Pro Leu His Ser Lys Ser Ser Arg Ile His Gln
1 5 10 15
Gln Ile Ile Val Gln Leu Asp Ser Leu Pro Pro Pro Val Phe Ser Glu
20 25 30
Gln Val Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu
35 40 45
Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr
50 55 60
Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln
65 70 75 80
Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln
85 90 95
Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser
100 105 110
Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg
115 120 125
Gln Leu Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr
130 135 140
Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg
145 150 155 160
Gln Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu
165 170 175
Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr
180 185 190
Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln
195 200 205
Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu
210 215 220
Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val
225 230 235 240
Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala
245 250 255
Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys
260 265 270
Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg
275 280 285

Glu	Glu	Leu	Ser	Arg	Ala	Phe	Ala	Gly	Thr	Gly	Thr	Glu	Glu	Gly	Ala
290						295					300				
Gly	Pro	Asp	Pro	Gln	Met	Leu	Ser	Glu	Glu	Val	Arg	Gln	Arg	Leu	Gln
305					310					315					320
Ala	Phe	Arg	Gln	Asp	Thr	Tyr	Leu	Gln	Ile	Ala	Ala	Phe	Thr	Arg	Ala
			325						330					335	
Ile	Asp	Gln	Glu	Thr	Glu	Glu	Val	Gln	Gln	Gln	Leu	Ala	Pro	Pro	Pro
		340						345					350		
Pro	Gly	His	Ser	Ala	Phe	Ala	Pro	Glu	Phe	Gln	Gln	Thr	Asp	Ser	Gly
	355						360					365			
Lys	Val	Leu	Ser	Lys	Leu	Gln	Ala	Arg	Leu	Asp	Asp	Leu	Trp	Glu	Asp
370					375					380					
Ile	Thr	His	Ser	Leu	His	Asp	Gln	Gly	His	Ser	His	Leu	Gly	Asp	Pro
385					390				395						400

<210> 42
 <211> 2128
 <212> DNA
 <213> Homo sapiens

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tcagcgtctg agccaggcca acaatgacca aggaggatgg gatcctgggt gcagctcatc	120
acaagcgtcg ggggtgcagca aaaccatcca ggctggacag tggctggaca gttccaagaa	180
aagaaacgct tcaactgaaga agtcattgaa tacttccaga agaaagttag cccagtgcac	240
ctgaaaatcc tgctgactag cgatgaagcc tggaagagat ttgtgcgtgt ggctgaattg	300
cccagggaag aggcagatgc tctctatgaa gctctgaaga atcttacacc atatgtgact	360
attgaggaca aagacatgca gcaaaaagaa cagcagttta gggagtgggt tttgaaagag	420
tttctctaaa tcagatggaa gattcaggag tccatagaaa ggcttcgtgt cattgcaa	480
gagattgaaa aggtccacag aggtgcgtc atcgccaatg tgggtgtctgg ctccactggc	540
atcctgtctg tcattggcgt tatgttggca ccatttacag cagggctgag cctgagcatt	600
actgcagctg gggtagggct gggaatagca tctgccacgg ctgggatcgc ctccagcatc	660
gtggagaaca catacacaag gtcagcagaa ctacagcca gcaggctgac tgcaaccagc	720
actgaccaat tggaggcatt aaggacatt ctgcatgaca tcacacccaa tgtgctttcc	780
tttgcacttg attttgacga agccacaaaa atgattgcga atgatgtcca tacactcagg	840
agatctaaag ccaactgttg acgccctttg attgcttggc gatatgtacc tataaatgtt	900
gttgagacac tgagaacacg tggggccccc acccgatag tgagaaaagt agcccggaac	960
ctgggcaagg ccaattcagg tgtccttggt gtgctggatg tagtcaacct tgtgcaagac	1020
tcactggact tgcacaaggg ggcaaaatcc gagtctgctg agtcgctgag gcagtgggct	1080

caggagctgg aggagaatct caatgagctc acccatatcc atcagagtct aaaagcaggc 1140
taggccaat tgttgcgga agtcaggac cccaaacgga gggactggct gaagccatgg 1200
cagaagaacg tggattgtga agatttcacg gacattttatt agttcccaa attaatactt 1260
ttataatttc ctatgcctgt ctttaccgca atctctaaac acaaattgtg aagatttcac 1320
ggacacttat cacttcccca atcaataccc ttgtgatttc ttatgcctgt ctttacttta 1380
atctcctaata cctgtcagct gaggaggatg tatgtcacct caggaccatg tgataattgc 1440
gttaactgca caaattgtag agcatgtgtg tttgaacaat atgaaatctg ggcaccttga 1500
aaaaagaaca ggataacagc aattgttcag ggaataagag agataacctt aaactctgac 1560
caacagttag cgggtggaa cagagtcata tttctcttct ttcaaaagca aatgggagaa 1620
atatcgctga attctttttc tcagcaagga acatccctga gaaagagaat gcaccctga 1680
gggtgggtct ataaatggcc tccttgggtg tggccatctt ctatggctga gactgtaggg 1740
atgaaataaa cccagctctc ccatagtgct cccaggctta ttaggaagag gaaattcccg 1800
cctaataaat tttggtcaga ccggttgctc tcaaaaccct gtctcctgat aagatgttat 1860
caatgacaat ggtgcctgaa acctcattag caattttaat ttctccccgg tcctgtggtc 1920
ctgtgatctc acctgcctc cacttgcctt gtgatattct attaccttgt gaagtaggtg 1980
atctttgtga cccacaccct attcatacac tccctccctt tttgaaagtc cctaataaaa 2040
acttgctggt tttgcagctt gtgaggcatc acggaaccta ctgatgtgtg atgtctcccc 2100
tggaacaccta gctttaaaat ttcaaaaa 2128

<210> 43
<211> 348
<212> PRT
<213> Homo sapiens

<400> 43
Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn
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His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe
20 25 30
Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
35 40 45
Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
50 55 60
Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
65 70 75 80
Lys Asn Leu Thr Pro Tyr Val Thr Ile Glu Asp Lys Asp Met Gln Gln
85 90 95
Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile
100 105 110

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Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn
    115                                120                                125

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser
    130                                135                                140

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe
    145                                150                                155                                160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly
    165                                170                                175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr
    180                                185                                190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser
    195                                200                                205

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro
    210                                215                                220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile
    225                                230                                235                                240

Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg
    245                                250                                255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu
    260                                265                                270

Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn
    275                                280                                285

Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn
    290                                295                                300

Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser
    305                                310                                315                                320

Ala Glu Ser Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn
    325                                330                                335

Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly
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<210> 44
<211> 988
<212> DNA
<213> Homo sapiens

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<222> (12)
<223> n = a, c, g, or t

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<220>
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 <223> n = a, c, g, or t

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 <223> n = a, c, g, or t

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 <223> n = a, c, g, or t

<220>
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 <223> n = a, c, g, or t

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 <223> n = a, c, g, or t

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 agctcacagt agcccgggcgg cccagggcaa tccgaccaca ttctactctc accgctgtag 120
 gaatccag atg cag gcc aag tac agc agc acg agg gac atg ctg gat gat 170
 Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp
 1 5 10
 gat ggg gac acc acc atg agc ctg cat tct caa gcc tct gcc aca act 218
 Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr
 15 20 25 30
 cgg cat cca gag ccc cgg cgc aca gtt ttt cag tac tac cag ctc tcc 266
 Arg His Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser
 35 40 45
 aat act ggt caa gac acc att tct caa atg gaa gaa aga tta gga aat 314
 Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn
 50 55 60
 acg tcc caa gag ttg caa tct ctt caa gtc cag aat ata aag ctt gca 362
 Thr Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala
 65 70 75
 gga agt ctg cag cat gtg gct gaa aaa ctc tgt cgt gag ctg tat aac 410
 Gly Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn
 80 85 90
 aaa gct gga ggc tat aca aga aac atg gtg cca gca tct gct tct tct 458
 Lys Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser
 95 100 105 110

gag agc ctc agg cag ctt cca cac atg ggg gaa agt gca gca gca cac	506
Glu Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His	
115 120 125	
agg tgc agc cct tgt aca gaa caa tgg aaa tgg cat gga gac aat tgc	554
Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys	
130 135 140	
tac cag ttc tat aaa gac agc aaa agt tgg gag gac tgt aaa tat ttc	602
Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe	
145 150 155	
tgc ctt agt gaa aac tct acc atg ctg aag ata aac aaa caa gaa gac	650
Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp	
160 165 170	
ctg gaa ttt gcc gcg tct cag agc tac tct gag ttt ttc tac tct tat	698
Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr	
175 180 185 190	
tgg aca ggg ctt ttg cgc cct gac agt ggc aag gcc tgg ctg tgg atg	746
Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met	
195 200 205	
gat gga acc cct ttc act tct gaa ctg ttc cat att ata ata gat gtc	794
Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val	
210 215 220	
acc agc cca aga agc aga gac tgt gtg gcc atc ctt aat ggg atg atc	842
Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile	
225 230 235	
ttc tca aag gac tgc aaa gaa ttg aag cgt tgt gtc tgt gag aga agg	890
Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg	
240 245 250	
gca gga atg gtg aag cca gag agc ctc cat gtc ccc cct gaa aca tta	938
Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu	
255 260 265 270	
ggc gaa ggt gac atg cat cat cat cat cat cat tagcctaggt tctagac	988
Gly Glu Gly Asp Met His His His His His His	
275 280	
<210> 45	
<211> 281	
<212> PRT	
<213> Homo sapiens	
<400> 45	
Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly	
1 5 10 15	
Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His	
20 25 30	
Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser Asn Thr	
35 40 45	

Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser
50 55 60

Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser
65 70 75 80

Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala
85 90 95

Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser
100 105 110

Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys
115 120 125

Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln
130 135 140

Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu
145 150 155 160

Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu
165 170 175

Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr
180 185 190

Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly
195 200 205

Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser
210 215 220

Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser
225 230 235 240

Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly
245 250 255

Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu
260 265 270

Gly Asp Met His His His His His His
275 280